

STIC Search Report Biotech-Chem Library

STIC Dalabase Therelong is a consistency

TO: Phuong Bui

Art Unit: 1638

Location: REM-2A15&2C18 Serial Number: 10/660226

Wednesday, August 31, 2005

From: Beverly Shears

Location: Biotech-Chem Library

REM 1A54

Phone: 571-272-2528

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Searca Notes

Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.



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T012132 SJN00015 SJN00015 SJN00094 P003585 E0017161 P006577 P006577 P006577 P005371 E001715 E001715 E001715 E001716 E000776 E0	BT009529 Triticum aestivum clone wrl.pk0122.a3:fis, full insert mRNA BGGGGEO BT009529 BT009529 BT009529 BT009529 BT009529 BT009529.1 GI:32129080 Triticum aestivum (bread wheat) Triticum aestivum (bread wheat) Triticum aestivum (breat will injustive in in in (bases in to 1061) Buraryora in	Location/Qualifiers
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VILL: http://cdnaol.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satch, K.,
NIAS Rice Full-Length cDNA Project Team: Kikuchi, S., Satch, K.,
Nadada, T., KawagaaBhira, N., Doi, K., Kishimoto, N., Yazaki, J.,
Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T.,
Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and
Yamamoto, M.
FAIS Genome Sequencing & Analysis Group: Otomo, Y., Iida, Y.,
Rujimura, T., Kursumegi, T., Lu, M., Manada, H.,
Nitawa, R., Naikura, J., Oka, M., Kyu, R., Sugano, S.,
Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, O., Yokomizo, S.,
Yoshimura, A., Matsubara, K. and Murakami, K.
Genome Exploration Research Group in Riken Genomic Sciences Center
and Genome Exploration Research Group in Riken: Adachi, J., Aizawa, K.,
Akimura, T., Arakawa, T., Carninci, P., Fuvuda, S., Hanagaki, T.,
Akimura, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K.,
Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y.,
Itoh, M., Kagwa, I., Kanagawa, S., Katch, H., Kawai, J.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Shinagawa, A., Shiraki, T.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Toya, T., Waki, K.,
Yasunishi, A., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
Yasunishi, A., Tanaka, Y., Tomaru, A., Toya, T., Waki, K.,
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Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M.,
Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J.,
Ikeda, R., Ishibiki, J., Kawamara, M., Yoshimura, A., Miura, J.,
Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN:
Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Flukuda, S.,
Haraa, A., Haabildume, W., Hayateu, N., Imocani, K., Ishi, Y., Itoh, M.,
Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y.,
Yoshino, M. and Hayashizaki, Y.
Yoshino, M. and Hayashizaki, Y.
Collection, mapping, and annotation of over 28,000 cDNA clones from
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AK109730 AK109730 1 G1:32994939 FLI_CDNA; oligo capping.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Ehrhartoideae; Oryzea; Oryzea; Oryzea.
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Oryza sativa (japonica cultivar-group) cDNA clone:J013074804, full
insert sequence.
AK066687
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                                                                                                                                          AGGTCATGAAAACTCGCACAACTCCGTTGACGAAGCTCTCCTGTTGAAGAAAAATCAGA
                                                                                                                                                          398 AGAAGTICTGTICTACTIGAACGGGAGGTGTATTTACCTAGTAGGAATGATGGCTICTGG
                                                                                                                                                                                                                                                                      CAAGTTAGTGGAGCAAGCTGTTGGAATGCCATCAGTTGCCCAAATATTCAAGGTCCATAG
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                                                                                                                                                                                                                     458 AAAAAGTACTGTGGGGAAGATTATGTCTGAAGTCTTGGGTTATTCGTTCTTTGATAGTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 698 GAGGGGCCTATCTGTTTGGTTAGATGTGCCCTTGGATGCTCTTGCTAGGCGTATTGCTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGTGGGAACTGCCTCTCCTCTTCTGGACCAACCATCTGGTGATCCGTACGCAATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     878 AAGGGTTTCTCTGGAAGAGATTGCATGTAAACAAGGTCATGATGATGTCTCTAAGCTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                           ATTAGTTGTTGCCACCGGAGGTGCTGTTATCCGACCAATTAACTGGAGATATATGAA
                                                                                                                Gaps
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m
                                                                                 Length 1918;
                                                                                                              Indels
                                                                                                              0; Mismatches 143;
                                                                                   DB 8;
                                                                                   41.8%; Score 501.2; DB 8 80.4%; Pred. No. 9.6e-101
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PLI CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
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/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="002-146-B12"
                                                                                              Best Local Similarity 80.4
Matches 600; Conservative
                                                                                                                                          338
                                                                                                                                                                                                                          1042
                                                                                                                                                                                                                                                                                                              518
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Shearyota, Viridiplanaes is treepophyte; Bmbryophyte; Trecheophyte; Bmbratcoldeae; Oryzas.

Burhartcoldeae; Oryzas.

Redening; Statement of International Conference of Manner and William Conference of Conference of William Con
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20-JUN-2003 mRNA

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Triticum aestivum

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticaea; Triticaea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  710 GAIGCCCGAGITICCCTIGAAATATIGCATICAAACAAGGACAIAAIGAIGIGAAIGIA 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          350 acrcanaacrocingacacrocicricacanacciccicciccicacaninini
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGACGATTAGTTGTTGCCACCGGAGGTGCTGCTGTTATCCGACCAATTAACTGGAGATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAGGCCTATGCCAAACTTACAGCACTTTTGAACAAAGAATGGATTCATATGCTAATGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATGTAAGGGTTTCTCTGGAAGAGATTGCATGTAAACAAGGTCATGATGATGTCTCTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTGGAAAAAGTACTGTGGGGAAGATTATGTCTGAAGTCTTGGGTTATTCGTTCTTTGAT
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  1323 bp mRNA linear PLN aestivum clone wrl.pk0099.bl2:fis, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Pred. No. 2.4e-70;
0; Mismatches 186;
                                                                                                                                                                                                                                                                                                                                                                                                                            1. .1323
|organism="Triticum aestivum"
|/mol_type="mRNA"
|db_xref="taxon:4565"
|clone="wrl.pk0099.b12:fis"
                                                                                      BT009514.1 GI:32129065
FLI CDNA.
Triticum aestivum (bread wheat)
                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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71.9%;
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    BT009514
Triticum
                                                sequence.
                                                                        BT009514
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Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,
Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Mateuvama, T., Miyazaki, A., Murata, M.,
Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N.,
Sasaki, D., Satoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H.,
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Sogabe, Y., Tagami, M., Tagami, Takeda, Y., Tagawa, A., Takahashi, F.,
Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K.,
Yasunishi, A. and Hayashizaki, Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  311 CCGACTCCGTGCGAAGAAATCGTCCGGAGGTCATGAAAACTCGCACAACTCCGTTGACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTACCTAGTAGGAATGATGGGTTCTGGAAAAAGTACTGTGGGGAAGATTATGTCTGAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTACCTAGTTGGAATGATGGGTTCTGGAAAAGTACTGTGGGAAAGATCATGTCTGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                      1. .1356
/organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/mol type="mRNA"
/db xref="taxon:39947"
/clone="J013074E04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                        47;
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                                                                                                                                                                                                                                                                                                                                                                                                         35.3%; Score 423.4; DB 8
79.6%; Pred. No. 1.8e-83;
iive 0; Mismatches 96
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Kirkness, E.F., Wang, W. and Vazeille, A. Direct Submission

Submitted (11-MAY-2004) The Institute for Genomic Research, 9712

Medical Center Drive, Rockville, MD 20850, USA

Location/Qualifiers
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                                                                                                                                                                                                  672 GGTGCAGTTGTTCGTCCCATTAATTGGAGCCATATGCCACAAGGGTATTAGTGTTTGGTTA
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                                                                                                                                                                                                                                                                                                                                                                      792 CTTTTACATGAAGAATCAGGAGACGTTTATGATACGACTTTGAAGCGGTTAACTACTTA
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                                      552 GGTGGAATTACTGTAGCTGAAATCTTTGAGCTTCGCGGAGAGAGGCTTCTTCAGGGATAAT
                                                                               600 GAGAGTAGTGTCTTGAGAGATTTGTCCTCCATGCGACGATTAGTTGTTGCCACCGGAGGT
                                                                                                                  ĠAĠAĊTĠAĠĊŢAŢŢĠCACAAAĊŢAŢĊŢŢŢĠŢĠĊAŢĊĠĊŢŢĠŢŢĠŢŢŢĊAĀĊĠĠŢĠĠA
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GGAATGCCATCAGTTGCCCAAATATTCAAGGTCCATAGTGAAGCCTTCTTTCGGGATAAT
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Pred. No. 3.4e-43;
0; Mismatches 231; Indels 3;
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/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/db_xref="taxon:4081"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="114107R"
/tissue type="mature green fruit"
/note="TMGHE47"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   960 TCACTICATAAGAICGAGAGCTICGICA 987
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VERSION
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TITLE
JOURNAL
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/product="shikimate kinase precursor"
/product="shikimate kinase precursor"
/product=101491
/db xref="GI:10349"
/db xref="GI:10349"
/db xref="GOA:000497"
/db xref="GOA:000497"
/db xref="miniprod.5wiss=-prod:000497"
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/translation="WEANYOSIGISSWINSDKVVRRPSGILRFSEKMNEKPRHRVVV
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DGRCVYLVAWGGCGKTTVGRILAETLGYSFPDCDRILEQAVGGITVARIFELRGESFP
RDNETEVLHKLSLAHRLVVSTGGGAVVRPINWRHMHKGISVWLDVPLEALAKRITTEG
TKSRPLLHESGGDVYDTTLARLTTAMETRGENYANASARVSLENIALKREKDVCHITP
AEITLEVLIQIENFLKTQKSVVVL"
                                                                                                                                                                                                                   X63560.1 GI:19348

shirimate kinase.
Lycopersicon esculentum (tomato)
Lycopersicon esculentum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.

E 1 (bases 1 to 123)
Schmid,J., Schaller,A., Leibinger,U., Boll,W. and Amrhein,N.
The in-vitro synthesized tomato shikimate kinase precursor is enzymatically active and is imported and processed to the mature
enzyme by chloroplasts
D plant J. 2 (3), 375-383 (1992)
                                                                                                                                                               PLN 16-JUN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (27-DEC-1991) A. Schaller, Federal Institute of
Technology, Institute of Plant Sciences, Sonnegstrasse 5, 8092
Zuerich, SWITZERLAND
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/mol_type="mRNA"
/strain="UC82b"
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/product="shikimate kinase"
/EC number="2.7.1.71"
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123. .1025
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Schaller, A.
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/note="compared to genomic sequence"
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                                                                                                  /mol_type="mRNA"
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                         Location/Qualifiers
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Seki, M., Iida, K., Satou, M., Sakurai, T., Akiyama, K., Ishida, J.,
Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Carninci, P.,
Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Carninci, P.,
Nawai, J., Hayashizaki, Y. and Shinozaki, K.

Direct Submission

Submitted (25-NOV-2002) Motoaki Seki, RIKEN Genomic Sciences
Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa
230-0045, Japan (E-mail:nmseki@spc.riken.go.jp,
URL:http://pfgweb.gsc.riken.go.jp, Tel:81-45-503-9625,
Fax:81-45-503-9586)

On Dec S. 2003 this sequence version replaced gi:26452805.
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al. (1998) Plant J. 15:707-720,
Seki et al. (2002) Science 296:141-145). cDNA cleaved with BamHI
and Xhol was ligated to modified Lambda FLC-1-E vector (Carninci et
al. (2001) Genomics 77:79-90) digested with BamHI and Sall.
This clone is in a modified pBluescript vector.

Please visit our web site (http://pfgweb.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AK118899 1300 bp mRNA linear PLN 14-FEB-2004 Arabidopsis thaliana At2g21940 mRNA for putative shikimate kinase precursor, complete cds, clone: RAFL21-24-A05.
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AKILL CDNA; CAP trapper.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Rujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M.,

Rodama, T., Kursoaki, T., Kusumegi, T., Lu, M., Mura, J.,

Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S.,

Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S.,

Yoshimura, A., Matsubara, K. and Murakami, K.

Genome Exploration Research Group in Riken: Adachi, J., Aizawa, K.,

Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T.,

Hara, A., Habhizume, W. Hayashida, K., Hayatsu, N., Hiramoto, K.,

Hiraoka, T., Hori, F., Ilda, J., Imamura, K., Imotani, K., Ishii, Y.,

Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J.,

Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,

Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,

Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N.,

Ota, Y., Saitoh, H., Sakai, C., Sakai, K., Sainagawa, A., Shiraki, T.,

Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,

Takaku-Akahira, S., Tanaka, T., Tomatu, A., Toya, T., Waki, K.,

Yasunishi, A., and Hayashizaki, Y.

Location Qualifiers

Location Qualifiers
                     Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
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Pred. No. 8.4e-39;
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="J023052021"
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Best Local Similarity 62.6%;
Matches 414; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The Rice Full-Length CDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length CDNA Project Team:, Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Otomo, Y., Murakami, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Murakami, K., Iida, Y., Sugayama, A., Mazuno, K., Yokomizo, S., Niikura, J., Kusumegi, T., Sugiyama, A., Mazuno, K., Yokomizo, S., Niikura, J., Kusumegi, T., Oka, M., Yawamata, M., Yoshimura, A., Mura, J., Kusumegi, T., Oka, M., Wayara, W., Matsubara, K., Riken, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayateu, N., Imchani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y. Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice
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Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Pujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Fujimura, T., Fukuda, S., Hanagaki, T., Hayaetsu, N., Hiramoto, K., Hiraoka, T., Hayashizaki, Y., Hayaetsu, N., Hiramoto, K., Hiraoka, T., Horta, I., Idida, J., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kowamata, M., Kakach, H., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kodawa, M., Kojima, Y., Kojima, Y., Kojima, Y., Miyazahi, M., Kodawa, T., Kishimoto, N., Kobayashi, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miyazaki, A., Mizuho, K., Murakami, K., Muraka, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Nikura, J., Nishi, K., Oka, M., Ooka, M., Osato, N., Cano, W., Sano, H., Sakai, C., Sakoi, K., Shibata, K., Shinata, K., Shinata, K., Shinata, K., Shinata, K., Shinata, K., Suzuki, Y., Susuh, M., Tagami, Takada, Y., Tuomaru, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yanaga, M., Waki, K., Xie, Q., Yahagi, W., Yanada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and
                                                                                                                                                                                                                         Oryconsol 1167 bp mRNA linear PLN 24-JUL-2003 Orycas sativa (japonica cultivar-group) cDNA clone:J023052021, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                    AKO7018.1 GI:32980142
FLI CDNA; CAP trapper.
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of
Agrobiological Sciences, Department of Molecular Genetics, Head of
Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
305-8602, Japan (B-mailsKikuchi@nias.affrc.go.jp,
Tel:81-29-838-7007, Fax:81-29-838-7007)
This clone is one of the 28K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  URL : http://cdna01.dna.affrc.go.jp/cDNA/
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SOURCE ORGANISM

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REFERENCE AUTHORS

TITLE JOURNAL

AUTHORS

TITLE JOURNAL

COMMENT

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/brotein_id="AAO63355.1"

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LLHDDESGDTYTAALNRLSTIWDARGEAYTKASARVSLENITLKLGYRSVSDLTPAEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGATCGATGTATCTTGTTGGTATGATGGGTTCCGGGAAAACGACTGTAGGGAAGATTATG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           355 GCAAGATCGCTTGGTTATACATTCTTTGATTGTGACACTTTGATCGAGCAGGCTATGAAG 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGAACTÍCTGTAGCTGAGATATTTGAGCATTTCGGTGAGAGTGTCTTCAGAGAAAAAGAG 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     780 CTTCTG---GACCAACCATCTGGTGATCCGTACGCAATGGCCTTTTCTAAGCTCAGCATG 836
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                715 ATTTGGGATGCACGTGGAGCATACACTAAAGCCAGCGCAAGAGTTTCCTTGGAGAAT 774
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  775 ATTACTTTGAAGCTCGGTTATAGAAGTGTCTCAGATCTTACACCAGCTGAAATCGCCATT 834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTGCTGTTATCCGACCAATTAACTGGAGATATATGAAGAGGGGCCTATCTGTTTGGTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GATGTGCCCTTGGATGCTCTTGCTAGGCGTATTGCTAAAGTGGGAACTGCCTCTCGTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 193; DB 8; Length 903;
Pred. No. 3.1e-32;
0; Mismatches 250; Indels
                                                                                                                                                                                                                                           'note="putative shikimate kinase"
                                                                                                                                                              in pUNI 51"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIEAFEOVOSYLEKEDGMARPDGL"
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xref="taxon:3702"
                                                                                                                                                                                                                                                                                          /codon_start=1
/product="At4g39540"
                                                                                                                   ecotype="Columbia"
                                                                                                                                                                  note="This clone"
                                                                                 'clone="U60448"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16.1%;
59.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 369; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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Eukaryotza; Virializalia

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases I to 903)

Kim, C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Carninci, P.,

Chan, M., Chang, C.H., Dale, J.M., Hayashizaki, Y., Hsuan, V.W.,

Ishida, J., Jones, T., Kanja, A., Karlin-Neumann, G., Kawai, J.,

nondera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M.,

Southwick, A., Tang, C.C., Toriumi, M., Nong, C., Wu, H.C., Yamada, K.,

Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Change I to 903)

Kim, C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Carninci, P., Chan, C.J., Chen, H., Dale, J.M., Hayashizaki, Y., Hsuan, V.W., Chan, M., Chang, C.H., Dalya, A., Karlin-Neumann, G., Kawai, J., Lahida, J., Jones, T., Kanlya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Ondera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLN 14-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Kim,C.J., Chen,H., Cheuk,R., Shinn,P., Bowser,L., Chan, M.M., Chang,C.M., Dale,J.M., Hsuan,V.W., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Miranda,M., Nguyen,M., Onodera, C.S., Palm,C.J., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yamada,K., Yu,G., Yuan,S., Davis,R.W., Theologis,A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kim, C.J. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs.
                                                                                     820 ATGCCAGGGTTTCACTCGAACATATTGCAGTGAAACAAGGACATAGTAATGTGACAC
                                                                                                                                                                                                                                                   ATGTAAGGGTTTCTCTGGAAGAGATTGCATGTAAACAAGGTCATGATGATGTCTTAAGC
                                                                                                                                                                                                        TGACACCTACTGATATTGCAATTGAGTCACTTCATAAGATCGAGAGCTTCGTCATCGAGC
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1. .903
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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Unpublished
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~ 422 294 482

Gaps

542

602

629 534 719 594 779 654 896

926

source

FEATURES

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/product="shikimate kinase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1002 ATTACTTTGAAGCTCGGTTATAGAAGTGTCTCAGATCTTACACCAGCTGAAATCGCCATT 1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cucumis sativus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I. Cucurbitales; Cucurbitaceae; Cucumis.

Kim, M.S., Yang, K.Y., Kim, Y.C. and Cho, B.H.
A shikimate kinase and an acidic peroxidase gene expression were primed by a rhizobacterial colonization upon challenge-inoculation with Corynespora cassicola in cucumber leaves
                                                                                                                                                                                                                                                          821
                                                                                                                                                                                                                                                                                                            779
                                                                                                                                                                                                                                                                                                                                                                                                            780 CTTCTG---GACCAACCATCTGGTGATCCGTACGCAATGGCCTTTTCTAAGCTCAGCATG 836
                                                                                                                                                                                                           GGTGCTGTTATCCGACCAATTAACTGGAGATATATGAAGAGGGGCCTATCTGTTTGGTTA 719
                                                                                                                                                                                                                                                                                                                                                           GATGTACCTCTAGAAGCCTTAGCGCATAGAATAGCTGCTGTAGGAACTGGTTCAAGACCA 881
                                                                                                                                                                                                                                                                                                                                                                                                                                                           882 riectracardargargicaggacacaracacacaccicriraaaccgrcrrraacg 941
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                                       642 GGAACTICTGIAGCTGAGATATITGAGCATTTCGGTGAGAGTGTCTTCAGAGAAAAAGGG
                                                                                                                                                         ACTGAAGCGTTAAAGAACTCTCTTTGATGTACCACCAAGTTGTTGTTTCAACCGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             837 CTTGCACAGCAAAGGGGTGATGCTTATGCAAATGCAGATGTAAGGGTTTCTCTGGAAGAG
          543 ATGCCATCAGTTGCCCAAATATTCAAGGTCCATAGTGAAGCCTTCTTTCGGGATAATGAG
                                                                                                          AGTAGTGTCTTGAGAGATTTGTCCTCCATG----CGACGATTAGTTGTTGCCACCGGAGGT
                                                                                                                                                                                                                                                          762 GGGGCAGTTATAAGACCCATCAATTGGAAGTACATGCATAAAGGTATTAGTATTTGGCTT
                                                                                                                                                                                                                                                                                                            GATGTGCCCTTGGATGCTCTTGCTAGGCGTATTGCTAAAGTGGGAACTGCCTCTCGTCCT
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2 (bases 1 to 1016)
Kim, M.S., Yang, K.Y., Kim, Y.C. and Cho, B.H.
Direct Submistion
Submitted (09-APR-2004) Applied Plant Science Division,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             וווה אאח mRNA linear Cucumis sativus shikimate kinase mRNA, partial cds.
AY596190

    1016
    organism="Cucumis sativus"

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<1._.474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al. (1998) Plant J. 15:707-720; Seki et al. (2002) Science 296:141-145). cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1-E vector (Carninci et al. (2001) Genomics 77:79-90) digested with BamHI and Sall. This clone is in a modified pBluescript vector.

Please visit our web site (http://pfgweb.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="putative shikimate kinase"
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LLHDDESGDTYTAAANLSTIWDARGBRYTKASARVSBLENITHKLGYRSVSDLTPABI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         422
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                                                                                                                                  Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTGACGAAGCTCCTCTTGAAGAGAAAATCAGAAGAAGTTCTGTTCTACTTGAACGGG
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                                                                                                                                                                                                                             Seki, M., Iida, K., Satou, M., Sakurai, T., Akiyama, K., Ishida, J.,
                                                                                                                                                                                                                                                                                                                                                                                     Ishida,J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center; 1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:mseki@gsc.riken.go.jp, URL:http://pfgweb.gsc.riken.go.jp, Tel:81-45-503-9586)
                                                                                                Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                        Seki M., Idda, K., Satou, M., Sakurai, T., Akiyama, K., Ishida, Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Carninci, P., Kamai, J., Hayashizaki, Y. and Shinozaki, K.
Direct Submission
Submitted (25-NOV-2002) Motoaki Seki, RIKEN Genomic Science
                                                                                                                                                                                                                                                     Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K. Arabidopsis thaliana full-length cDNA Published Only in Database (2002)
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llarity 59.0%; Pred. No. 3.3e-32;
Conservative 0; Mismatches 250;
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/note="common name: thale cress"
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                          AK117791.1 GI:26450650
FLI CDNA; CAP trapper.
Arabidopsis thaliana (thale cress)
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URE: http://cdnaol.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Namiki,T.,
Ishikawa,M., Yaanada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yaahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
FAIS Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y.,
Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,H., Miura,J.,
Mizuno,K., Narikawa,T., Tsumoda,Y., Ueda,M., Ryu,R., Sugano,S.,
Sugiana,A., Batsukaya,R., Nilkura,J., Oda,M., Ryu,R., Sugano,S.,
Sugiana,A., Matsubara,K. and Murakami,K.
Genome Exploration Research Group in Riken: Adachi,J., Aizawa,K.,
Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hayamoto,K.,
Hiraoka,T., Hori,F., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,
Itoh,M., Kagawa,I., Kanagawa,S., Karoh,H., Kawai,J.,
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Nakamura,M., Nishi,K., Nomira,K., Numasaki,R., Ohno,M., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Saro,H.,
Sasaaki,D., Sato,K., Shibata,K., Numasaki,R., Ohno,M., Sano,H.,
Sogabe,Y., Tanami,A., Toya,T., Waki,K.,
Yasunishi,A., and Hayashizaki,Y.
              Loudenty, J., Alzawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Fujimura, T., Fukuda, S., Hanagaki, T., Hayateu, N., Hiramoto, K., Hiraoka, T., Hayateu, N., Hiramoto, K., Hiraoka, T., Horta, I., Iida, J., Iida, Y., Ikeda, R., Imamura, K., Horta, I., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kiuchh, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodam, T., Kojima, K., Kojima, Y., Mutura, J., Miyazaki, A., Masuda, H., Matsubara, K., Matsuyama, T., Namura, M., Manada, M., Nagata, T., Nakamura, M., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Nomura, K., Sakai, K., Sakai, C., Sakai, K., Sakai, C., Sakai, C., Sakai, C., Sakai, M., Sano, H., Sasaki, D., Sato, K., Satoh, K., Tagama, A., Suzuki, K., Suzuki, T., Tagama, M., Tagami, M., Tagami, M., Tagama, T., Tomaru, A., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Vanisha, S., Vanishi, M., Yazaki, J., Yokomizo, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@mas.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
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69.8%; Pred. No. 8.3e-26;
tive 0; Mismatches 96;
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/cultivar="Nipponbare"
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/clone="J013123F09"
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Best Local Similarity 69.8
Matches 222, Conservative
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Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAAGGTCATGATGTCTCTAAGCTGACACCTACTGATATTGCAATTGAGTCACTTCAT 968
                                                                                                                                                                                                                                                                                                                                         67 GCATTGAGGAAGTTATCTTTGATGCGCCAGTTTGTTATTTCCACAGGCGGAGGTGCTGTA 126
                                                                                                                                                                                                                                                                                                                                                                                                             669 ATCCGACCAATTAACTGGAGATATATGAAGAGGGGCCTATCTGTTTGGTTAGATGTGCCC 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   729 ITGGATGCTCTTGCTAGGCGTATTGCTAAAGTGGGAACTGCCTCTCTCGTCCTCTTCTGGAC 788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          849 AGGGGTGATGCTTATGCAAATGCAGATGTAAGGGTTTCTCTGGAAGAGATTGCATGTAAA 908
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                                                                                                                                                                                                      7 TCTGTAGCCGAAGTTTTCAAGGTCTATGGGGAGGACTTCTTTAGAGAAAGGGAGACGGAA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    969 AAGATCGAGAGCTTCGTCATCGAGCACACTGCTGATAGTTCAGCTAGCGACGCGCAA 1025
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                                                                                                                                      549 TCAGTTGCCCAAATATTCAAGGTCCATAGTGAAGCCTTCTTTCGGGATAATGAGAGTAGT
                                                                                                                                                                                                                                                                      609 GTCTTGAGAGATTTGTCCTCCATGCGACGATTAGTTGTTGCCACCGGAGGTGGTGTTT
                                                                      Gaps
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0
   Length 1016;
                                                                   Indels
Score 185.8; DB 8;
Pred. No. 1.3e-30;
0; Mismatches 182;
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AK067948.1 GI:32977966
Query Match
Best Local Similarity 61.8%;
Matches 295; Conservative
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AK067948
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Submitted (22-AUG-2011) Takuji Sasaki, National Institute of Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mai:tesasaki@mias.affrc.go.jp, VRL:http://rgp.dna.affrc.go.jp/, Tel:81-228-38-7441, Fax:81-229-38-7468)

Tel:81-228-38-7441, Fax:81-299-38-7468)

Tel:81-229-38-7441, Fax:81-299-38-7468)

The nuclocitide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
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                                AP004089 111777 bp DNA linear HTG 21-MAR-2002 Oryza sativa (japonica cultívar-group) chromosome 2 clone OJ1308_A10, *** SEQUENCING IN PROGRESS ***.
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Oryza satīva (japonica cultivar-group)
Oryza satīva (japonica cultivar-group)
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTAACTGGAGATATATGAAGAGGGCCTATCTGTTTGGTTAGATGTGCCCTTGGATGCT
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/mol_type="genomic DNA"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                           BAC
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2,
clone:OJ1308_A10
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                                                                                                                                                                                                                                                                                                                                                                 Sasaki,T., Matsumoto,T. and Yamamoto,K.
Direct Submission
                                                                                                                                                                                                                                                                                                                             Published Only in Database (2001)
2 (bases 1 to 111777)
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/chromosome="2"
/clone="0J1308_A10"
                                                                                                                  GI:15281368
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Best Local Similarity 86.4
Matches 133; Conservative
                                                                                                                                    HTG; HTGS_PHASE2
                                                                                                                AP004089.1
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RESULT 14
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VERSION
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TITLE
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AP004774
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                                                                                                        1704 TGGTGATCCTTATGCAAAGGCTTATGCAAACTGACTGCACTTTTTGAACAAAGAATGGA 1763
                          1764 CTCATATGCTAATGCTGATGCCAGGGTTTCACTCGAACATATTGCAGTGAAAGAAGGACA 1823
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
857 IGCTTATGCAAATGCAGATGTAAGGGTTTCTCTGGAAGAGATTGCATGTAAACAAGGTCA
                                                                                                                                                                                                                                917 TGATGATGTCTCTAAGCTGACACCTACTGCATATTGCAATTGAGTCACTTCATAAGATCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGTGATCCGTACGCAATGGCCTTTTCTAAGCTCAGCATGCTTGCACAGGCAAAGGGGTGA
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Human polynucleotides and polypeptides encoded thereby
Patent: WO 0190366-A 8601 29-NOV-2001;
Curagen Corporation (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.1%; Score 157; DB 6; Length 309;
69.3%; Pred. No. 2.6e-24;
iive 0; Mismatches 95; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8601 from Patent W00190366.

    .309
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

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                                                                                                                                                                                                                                                                                                                                             1884 GAGCTTTCTTACTGAGAA 1901
                                                                                                                                                                                                                                                                                                           977 GAGCTTCGTCATCGAGCA 994
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AX315616.1 GI:17899043
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Best Local Similarity
Matches 214; Conserv
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AUTHORS
TITLE
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/ trainiation="MMSISVEAAARDSLSDDKELIRTYERLTALDGKRRFALAAAAS
HEREVGRIERFFEDVDRSWETERALMGHYTWFERLSKDSPGTULARLARVUEMOELLD
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QOVAERAARTOMATIANGTRTANKGGGGATGTPRSTODKSKYGGKGYKOKCYE
IRKAVEARFDKLLITELVFSEDLMEALEBAKAIGDELGDIYDVVAPCFPPRYEIFQLMV
LYTTRRFQMATLAGTRANDIPHINITLKYTGWYWYKQENLIGGKUDESLAQVCSESGA
LUDPLAMMAYUERMQATTKKWYSNILEADKTQPPRSTEDGKLYTPAAVDLFRILTGQVOI
VTENSTDVMLYRIALAAVIQVMLDFQAARQRLEEPASDVGLESLCALINNNLRCYELS
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KDWMSGAWYERLQORFADYFQPRSTRYGACLEOTIVVYUDHLITQKGYH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement join (10085. 10456,10633. 10695,10796. 10912, 11113. 11202,11457. 11544,12002. 12091,12505. 12583, 113791. 118385,14487. 14573,14661. 14744,14864. 15043, 15122. 12526,15433. 15541,15971. 16026,16437. 16484, 16581. 16719,17270. 17377,17698. 17724,17885. 17977, 18397. 18476,18611. 18700,18846. 18936,19063. 19354, 796ne."P0431806,5."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .10912
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complement(join(10325. 10456,10633. 10695,10796. 10912

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13791. 11335,14487. 14573,44661. 14744,14644.

15122. 15262,1487. 14573,4661. 14744,14644.

16581. 16719,17270. 17377,17698. 17724,17885. 17977,

18397. 18476,18611. 18688)

/gene="PO4411806.5"

/note="contains EST(s): AU069794(E3332)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="P0431B06.3"
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                                                                                                                                                                                                                                  note="contains full-length cDNA(s): AK058832"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="P0431B06.3"
complement'
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                                                          complement (4342. .4808)
/gene="P0431B06.2"
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                                                                                                                                                                        complement (4442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agrobalogical Sciences, Rice Genome Research Program; Kannondai 21-2; Tsukuba, Ibaraki 305-8602, Japan
2-1-2; Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tessaki@nias.affcr.go.jp, URL:http://rgp.dna.affcr.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)

On Apr 14, 2004 this sequence version replaced gi:33468820.
Genes were predicted from the integrated results of the following:
GENSCAN (http://cor.ed.). Girm. the integrated results of the following:
(http://www.tigr.org/cdb/gilmerm/gilm.form.html), FGENESH
(http://www.tigr.org/cdb/gilmerm/gilm.form.html), FGENESH
(http://polal.biology.gatech.edu/GeneWark/), GilmmerM
(http://ploinformatics.isatate.edu/cgilb.ing.dorm.html), Gap2
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(http://ploinformatics.isatate.dors/sim.html), gap2
(http://ploinformatics.isatate.dors/sim.html), gap2
(http://ploinformatics.ing.ntml)

Gequence database at RGP or DDBJ. Protein homologics of the coding
regions were searched against NGBI NonRedundant Protein database
with BLASTP. ESTs represent the identified cDNA sequences using
BLASTN with the corresponding DDBJ accession no. and RGP clone ID.
Pull-length cDNAs represent the identified cDNA sequences using
squence database at RGP or significant homology to a protein a gene prediction program is also classified as a
classified based on the protein but with full-length of partial
squences as ame name, 'putative' and 'like perform' perform' protein accession no.
A gene with identity or significant homology (covering almost the entire length of partial
squence is classified as an 'unknow' protein. A gene predicted by a single gene prediction pr
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3141. .>3402)
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                              Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (20-FEB-2002) Takuji Sasaki, National Institute of
                                                                                                                                                                                                Sasaki,T., Matsumoto,T. and Yamamoto,K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, PAC
clone:P0431B06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Oryza sativa (japonica cultivar-group)"
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(cultivar="Nipponbare"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="supported by full-length cDNA(s): AK066687"
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/note="contains full-length cDNA(s): AK066687
                                                                                                                                                                                                                                                                                                                                                                 Sasaki,T., Matsumoto,T. and Yamamoto,K. Direct Submission
                                                                                                                                                                                                                                                                                                Published Only in Database (2002)
2 (bases 1 to 154796)
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                                                                                                                                      Ehrhartoideae; Oryzeae; Oryza.
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747. .3402
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EHQPDCPPEVVEKLVGMREGI PRKEAKEVVQECKEI YENSLVDGNPQKSGFVFGKLKC
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10.0%; Score 120.4; DB 8; Length 154796;
Best Local Similarity 86.4%; Pred. No. 1.1e-15;
Matches 133; Conservative 0; Mismatches 21; Indels 0;
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. OM nucleic - nucleic search, using sw model	Run on: August 25, 2005, 12:54:01 ; Search time 726 Seconds (without alignments) 9784.696 Million cell updates/sec	Title: US-10-660-226-9 Perfect score: 1200 Sequence: 1 ccgccaccagctaccctgccaaaaaaaaaaaaaa	Scoring table: IDENTITY_NUC Gapop 10.0 , Gapext 1.0	Searched: 4390206 segs, 2959870667 residues	um DB seq length: 0 um DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	eq_16De seq_16De seq_16De seq_16De seq_1200 seq_120

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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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.larity 62.4%; Pred. No. 1.9e-45;
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25 - MAY - 1999;
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677 CTGGAAGTATATGCATAAAGGAATCAGCATTTGGCTAGATGTGCCTCTAGAAGCATTAGC 736
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                                                          TGCAAATGCAGATGTAAGGGTTTCTCTCGGAAGAGATTGCATGTAAACAAGGTCATGATGA
                                                                                            CACAAACGCAAATGCCAGAGTCTCCTTAGAAATATTGCAGCAAGCGTGGCTATAAAA
                                                                                                                          TGTCTCTAAGGTGACACCTACTGATATTGCAATTGAGTCACTTCATAAGATCGAGAGCTT
               TCCGTACGCAATGGCCTTTTCTAAGCTCAGGATGCTTGCACAGCAAAGGGGGTGATGCTTA
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09-MAR-1999;
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RR 06-AUG-1999; 99US-014743EP.
RR 10-AUG-1999; 99US-014743EP.
RR 11-AUG-1999; 99US-014743EP.
RR 11-AUG-1999; 99US-0148119P.
RR 12-AUG-1999; 99US-0148119P.
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RR 12-AUG-1999; 99US-0148119P.
RR 12-AUG-1999; 99US-0148119P.
RR 20-AUG-1999; 99US-0149725P.
RR 20-AUG-1999; 99US-015066F.
RR 20-AUG-1999; 99US-015106F.
RR 20-AUG-1999; 99US-0151070P.
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                                                             Gaps
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                                    Length 1491;
                                 Query Match 19.7%; Score 236.8; DB 3; Length Best Local Similarity 62.2%; Pred. No. 8.9e-45; Matches 373; Conservative 0; Mismatches 227; Indels
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16-JUL-1999; 16-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999;	19-JUL-1999; 20-JUL-1999; 20-JUL-1999; 20-JUL-1999; 21-JUL-1999;	21-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 23-JUL-1999; 23-JUL-1999;	25-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999; 28-JUL-1999; 02-AUG-1999; 02-AUG-1999; 02-AUG-1999;	04-ANG-1999; 06-ANG-1999; 05-ANG-1999; 06-ANG-1999; 06-ANG-1999; 09-ANG-1999; 09-ANG-1999; 11-ANG-1999; 11-ANG-1999; 11-ANG-1999; 13-ANG-1999;	16-AUG-1999; 17-AUG-1999; 18-AUG-1999; 20-AUG-1999; 20-AUG-1999; 23-AUG-1999; 25-AUG-1999; 25-AUG-1999; 27-AUG-1999; 27-AUG-1999; 27-AUG-1999;	30-AUG-1999; 31-AUG-1999; 31-AUG-1999; 07-SEP-1999; 10-SEP-1999; 16-SEP-1999; 20-SEP-1999; 22-SEP-1999; 24-SEP-1999; 24-SEP-1999; 24-SEP-1999; 24-SEP-1999; 26-OCT-1999; 66-OCT-1999;
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The invention comprises DNA sequences which confer an altered metabolic characteristic when they are expressed in a plant. The DNA sequences of the invention are useful for producing plants with an altered metabolic characteristic, such as: altered acid metabolism, alcohol metabolism, altered detabolism, altered detabolism, altered phenolic metabolism, altered phenolic metabolism, altered phenolic metabolism, altered phenolic metabolism, altered seter metabolism, altered sterol, oxygenated terpene, or isoprenoid metabolism, con quinone metabolism. The DNA sequences of the invention may be used to provide disease resistance in a plant and gene shuffling or sexual PCR procedures. The present nucleic acid represents a DNA sequence of the invention.
Novel genes that confer altered metabolic characteristics in Nicotiana benthamiana plants, useful for altering the levels of metabolites e.g. acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
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                                                                                                                                                                                                                                                                                       Plant DNA sequence which confers altered metabolic characteristic #57
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Reddy AS, Shukla V, Larrinua I, Miller
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branched fatty acid metabolism; alkaloid metabolism;
amino acid metabolism; ester metabolism; glyceride metabolism;
phenolic metabolism; carbohydrate metabolism; sterol metabolism;
terpene metabolism; isoprenoid metabolism; alkene metabolism;
alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
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Pred. No. 3.8e-44;
0; Mismatches 209; Indels 3;
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(DOWC ) DOW AGROSCIENCES LLC.
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Matches 372; Conservative
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Crosley R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          372 TCAAGAGAAAAGCAGAAGAGGTTAAACCGTATTTGAATGGACGATCTATGTACCTTGTCG 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGTTCTTTGATAGTGACAAGTTAGTGGAGCAAGCTGTTGGAATGCCATCAGTTGCCCAAA 561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAATGATGGGTTCTGGGAAACAACTGTGGGAAAGTTAATGTCCAAAGTGCTCGGTTATA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATTCAAGGTCCATAGTGAAGCCTTCTTTCGGGATAATGAGAGTAGTGTCTTGAGAGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATTTGTTCATCACGGAGAGATTTTTTAGAGGAAAGGAGGACCGATGCGCTTAAGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTOGRAGIATATGCATAAAGGAATCAGCATTTGGCTAGATGTGCCTCTAGAAGCATTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCCATAGAATCGCTGCTGTTGGAACTGATTCACGACCACTGCTACACGATGAATCAGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGCAAATGCAGATGTAAGGGTTTCTCTGGAAGAGATTGCATGTAAACAAGGTCATGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAATGATGGGTTCTGGAAAAGTACTGTGGGGAAGATTATGTCTGAAGTCTTGGGTTATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     382 TGAAGAGAAAATCAGAAGAAGTTCTGTTCTACTTGAACGGGAGGTGTATTTACCTAGTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTGGAGATATATGAAGAGGGGCCTATCTGTTTGGTTAGATGTGCCCTTGGATGCTCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGTTCTTTGACTGCGACACTTTGATTGAACAGGCGATGAATGGAACTTCTGTTGCAGAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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Pred. No. 1.2e-44;
0; Mismatches 228;
                                                                                                                                                                                                                                                                                                                                                                                                                990S-0161406P
990S-0161359P
990S-0161360P
990S-0161920P
990S-0161920P
990S-0161992P
990S-0161993P
99US-0158029P.
99US-0158232P.
99US-0158369P.
99US-0159294P.
99US-0159295P.
99US-0159295P.
99US-0159339P.
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9903-0159638P.
9903-0159584P.
9903-0160741P.
9903-0160767P.
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990S-0160818P.
990S-0160981P.
990S-0160981P.
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62.1%;
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Best Local Similarity
Matches 373; Conser
                                                    13-0CT-1999;
13-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
14-0CT-1999;
18-0CT-1999;
18-0CT-1999;
18-0CT-1999;
18-0CT-1999;
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21-OCT-1999;
22-OCT-1999;
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67 - MAX - 1999;
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19-JUL-1999;
20-JUL-1999;
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   248
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                                                                                                                                                                                                                                                                                                         GITIGETTAGATGITCCTTTAGATGCTTTGGCCAAGAGAGTTACTGCTGAAGGAACTAAA 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 950
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9 TATCTAGATGGACGATGTATATACCTCGTTGGAGTGATGGGCTCTGGCAAAACAACTGTG
                                                 591 CGGGATAATGAGAGTAGTGTCTTGAGAGATTTGTCCTCCATGCGACGATTAGTTGTTGCC
                                                                                                                                                                               651 ACCGGAGGTGCTGTTATCCGACCAATTAACTGGAGATATATGAAGAGGGGCCTATCT
                                                                                                                                                                                                                                             TCTCGTCCTCTTCTGGACCAACCATCTGGTGATCCGTACGCAATGGCCTTTTCTAAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                                 AGCATGCTTGCACACCAAAGGGGGTGATGCTTATGCAAATGCAGATGTAAGGGTTTCTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAGAGATTGCATGTAAACAAGGTCATGATGTGTCTCTAAGCTGACACCTACTGATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGAAGATTATGTCTGAAGTCTTGGGTTATTCGTTCTTTGATAGTGACAAGTTAGTGGAG
                                                                                              CAAGCTGTTGGAATGCCATCAGTTGCCCAAATATTCAAGGTCCATAGTGAAGCCTTCTTT
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99US-0123180P.
99US-0125348P.
99US-0126264P.
99US-0126785P.
99US-0128234P.
99US-0128445P.
99US-0128445P.
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05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
16-APR-1999;
119-APR-1999;
21-APR-1999;
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                               471
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9905-0144632P

9905-0144884P

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9905-014511P

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9905-014508BP

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9905-015130BP

9905-015332BP

9905-0159233BP

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30-JUL-1999;
31-JUL-1999;
31-JU
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721 TATTTGTTCATCACGGAGAGAATTTTTTAGAGGAAGGAGGACGGATGCGCTTAAGAAGC 780 CGTTCTTTGATAGTGACAAGTTAGTGGAGCAAGCTGTTGGAATGCCATCAGTTGCCCAAA 862 AIGCAAAIGCAGAIGIAAGGIITCICIGGAAGAGAITGCAIGIAAACAAGGICAIGAIG TATTCAAGGTCCATAGTGAAGCCTTCTTTCGGGATAATGAGAGTAGTGTCTTGAGAGATT ATCCGTACGCAATGGCCTTTTCTAAGCTCAGCATGCTTGCACAGGCGAAAGGGGGTGATGCTT 922 AIGICTCTAAGCIGACACCTACTGATATTGCAATTGAGTCACTTCATAAGATCGAGAGCT TGTCCTCCATGCGACGATTAGTTGTTGCCACCGGAGGTGGTGCTGTTATCCGACCAATTA 382 IGAAGAGAAAATCAGAAGAAGTICIGITCIACTIGAACGGGAGGIGIAITIACCIAGIAG Gaps .. Score 227; DB 3; Length 1484; Pred. No. 1.7e-42; 0; Mismatches 225; Indels 99US-0159637P.
99US-0159638P.
99US-0160741P.
99US-0160767P.
99US-0160768P.
99US-0160814P.
99US-0160814P.
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99US-0161981P.
99US-0161936P.
99US-0161361P.
99US-0161361P.
99US-0161361P.
99US-0161361P.
99US-0161361P.
99US-0161361P.
99US-0161361P. Query Match
18.9%;
Best Local Similarity 62.2%;
Matches 374; Conservative 0 r 1141 T 982 14-0CT-1999; 14-0CT-1999; 18-0CT-1999; 21-0CT-1999; 21-0CT-1999; 21-0CT-1999; 21-0CT-1999; 22-0CT-1999; 22-0CT-1999; 25-0CT-1999; 25-0CT-1999; 26-0CT-1999; 982 663 562 622 742 802 502 d 셤 g 원 g ð g ò g à 셤 ò ð 셤 ò 셤 ઠે ઠે à ò ठ

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RESULT

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990S-0139460P
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                                                                                                                                                                              Gaps
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                                                                                                                                                        15.1%; Score 181; DB 3; Length 1093; 58.9%; Pred. No. 7e-32;
                                                                                                                                                                             Indels
                                                                                                                                                                             0; Mismatches 250;
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99US-0160814P.
99US-0160815P.
99US-016080P.
99US-016088P.
99US-0161404P.
99US-0161404P.
99US-0161406P.
99US-0161359P.
99US-0161350P.
99US-0161350P.
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                                                                                                                                                                              Conservative
                                                                                                                                                                     Similarity
 21-0CT-1999;
22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
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Matches 368;
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99US-01406353P-
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99US-0140635P-
99US-0140635P-
99US-0141287P-
99US-014280P-
99US-014281P-
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99US-014281P-
99US-014281P-
99US-014281P-
99US-014331P-
99US-0144331P-
99US-01443331P-

22 - 70N - 1999;
23 - 70N - 1999;
24 - 70N - 1999;
28 - 70N - 1999;
29 - 70N - 1999;
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32 - 70N - 1999;
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36 - 70N - 1999;
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03-AUG-1999;
04-AUG-1999;
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05-AUG-1999;
06-AUG-1999;
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09-AUG-1999

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14-AUG-1999

16-AUG-1999

17-AUG-1999

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27-AUG-1999;
27-AUG-1999;
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163 558

Gaps

9

3; Length Indels

Score 166.6; DB 3; Pred. No. 1.3e-28; 0; Mismatches 219;

0;

13.9%; Similarity 59.0%; 4; Conservative (

Local Sim 439

Query Match Best Loca Matches 499 164

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AAATATTCAAGGTCCATAGTGAAGCCTTCTTTCGGGATAATGAGAGTAGTGTCTTGAGAG ATTIGICCTCCATG---CGACGATTAGTTGTTGCCCCCCGGAGGTGGTGCTGTTATCCGAC

224

619 284 919 344

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559

CCATCAATTGGAAGTACATGCATAAAGGTATTAGTATTTGGCTTGATGTACCTCTAGAAG

Aacrcrcrrrcargraccaccaagrrgrrgrrcaaccggggagggggggrraraagac CAATTAACTGGAGATATATGAAGAGGGGCCTATCTGTTTGGTTAGATGTGCCCTTGGATG

618 283 675 343 735 403

990S-0151303P 990S-0151438P 990S-015303P 990S-015303P 990S-015303P 990S-015403P 990S-015403P 990S-015403P 990S-015659P 990S-015659P 990S-015659P 990S-015659P 990S-015659P 990S-015659P 990S-015639P 990S-015923P 990S-015923P 990S-015923P 990S-0159294P 990S-0159294P 990S-0159294P 990S-0159294P 990S-0159294P 990S-016931P 990S-016932P 990S-0161361P 990S-0161361P 990S-0161361P 990S-0161361P 30-AUG-1999; 31-AbG-1999; 01-SEP-1999; 10-SEP-1999; 13-SEP-1999; 15-SEP-1999; 16-SEP-1999; 22-SEP-1999; 22-SEP-1999; 29-SEP-1999 04-0CT-1999 06-0CT-1999 13-0CT-1999 13-0CT-1999 14-0CT-1999 14-0CT-1999 14-0CT-1999 14-0CT-1999 14-0CT-1999 14-0CT-1999 12-0CT-1999 22-0CT-1999 22-0CT-1999 22-0CT-1999 23-0CT-1999 25-0CT-1999 26-0CT-1999

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BP
                                       DNA sequence of the invention.
                                                                                         13.6%;
70.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                       Matches 217; Conservative
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                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        GTTGCCA
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CTCTTGCTAGGCGTATTGCTAAAGTGGGAACTGCCTCTCGTCC---TCTTGTGGACCAAC 792
                         ccrinaccecaracannacionacidascancicaricascancerreciarente atos
                                                                                                                                                                                        GTTATAGAAGTGTCTCAGATCTTACACCAGCTGAAATCGCCATTGAGGCCTTTGAGCAAG 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention comprises DNA sequences which confer an altered metabolic characteristic when they are expressed in a plant. The DNA sequences of the invention are useful for producing plants with an altered metabolic characteristic, such as: altered acid metabolism, alcohol metabolism, fatty acid metabolism, branched fatty acid metabolism, alkaloid or other base metabolism, altered amino acid metabolism, altered ester metabolism, altered amino acid metabolism, altered ester metabolism, altered station acid metabolism, altered station acid metabolism, altered station acid metabolism, altered station, oxygenated terpene, or isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       benthamiana plants, useful for altering the levels of metabolites e.g. acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
                                                                                                                                                                                                                                                                                                                                                                                              Plant DNA sequence which confers altered metabolic characteristic #5640.
                                                                                                                                                                                                                                                                                                                                                                                                                 altered metabolic characteristic; plant; acid metabolism; alcohol metabolism; fatty acid metabolism; branched fatty acid metabolism; alkaloid metabolism; anino acid metabolism; ester metabolism; glyceride metabolism; phenolic metabolism; carbohydrate metabolism; sterol metabolism; terpene metabolism; carbohydrate metabolism; alkene metabolism; alkyne metabolism; hydrocarbon metabolism; ketone metabolism; quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blakeslee B, Mccreary DA, Pell RJ;
Reddy AS, Shukla V, Larrinua I, Miller BA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel genes that confer altered metabolic characteristics in Nicotiana
                                                                                                                                    Grichadocariacactradadeceadeceadearirrecriogadaarariactrirgaadered
                                                                                464 AGTCAGGGGACACATACACAGGGCTTTAAACCGTCTTTCAACGATTTGGGATGCACGTG
                                                                                                          GTGATGCTTATGCAAATGCAGATGTAAGGGTTTCTCTGGAAGAGATTGCATGTAAACAAG
                                                                                                                                                                GTCATGATGATGTCTCTAAGCTGACACCTACTGATATTGCAATTGAGTCACTTCATAAGA
                                                     CATCTGGTGATCCGTACGCAATGGCCTTTTTCTAAGCTCAGCATGCTTGCACAGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 5640; 2576pp; English.
                                                                                                                                                                                                                                                                                                               ADK58257 standard; DNA; 660 BP.
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(DOWC ) DOW AGROSCIENCES LLC.
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Crosley 1
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Oriedo JVB,
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metabolism, ketone or quinone metabolism. The DNA sequences of the invention may be used to provide disease resistance in a plant and gene shuffling or sexual PCR procedures. The present nucleic acid represents a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; ORF; open reading frame; ORFX; drug screening; diagnosis; disease monitoring; cytokine; cell proliferation; cell differentiation; immune modulation; hamatopoiesis regulation; tissue growth; angiogenesis; activin; inhibin; chemocractic; chemokinetic; haemostatic; thrombolytic; tumour inhibition; bodily characteristic; fertility; behaviour; cancer; proliferative disorder; neurological disorder; cardiovascular disease; immune system disorder; organ transplantation; tissue growth disorder; tissue regeneration disorder; diabetes mellitus; hypothyroidism; cholesterol ester storage disease; infection; vulnerary; vasotropic; antipsoriatic; antidiabetic; cytostatic; nootropic; neuroprotective; antidiabetic; cytostatic; nootropic; cardiant; hypotenaive; antibityroid; antidiamantory; immunomodulator; dermatological; analgesic; virucide; antibacterial; fungicide; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGAAAAGTCGCGGTTTAGTTGACGAGCCTTCCATTTTGAAGAAAAATCTCAAGATGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTGTTCTACTTGAACGGGAGGTGTATTTACCTAGTAGGAATGATGGTTCTGGAAAAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTCTTTCGGGATAATGAGAGTAGTGTCTTGAGAGATTTGTCCTCCATGCGACGATTAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAAAACTCGCACAACTCCGTTGACGAAGCTCTCCTGTTGAAGAAAAATCAGAAGAAGTT
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                 Length 660;
                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                    Sequence 660 BP; 194 A; 74 C; 168 G; 224 T; 0 U; 0 Other
                                                                                                                                                                                                                                                                                                                                                                                 90;
                                                                                                                                                                                                                                                                                                 Score 163; DB 10;
Pred. No. 8.9e-28;
0; Mismatches 90;
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P-PSDB; ABP35328

Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ transplantation.

Claim 1; Page 2393; 2508pp; English.

Compared DRAY 1021 represent 4524 and sequences ABN75054
ABN79587 represent cDNAs encoding them. The invention also encompasses

DAN79587 represent cDNAs encoding them. The invention also encompasses

DAN79587 represent cDNAs encoding them. The invention also encompasses

DAN79587 represent cDNAs encoding them. The invention also encompasses

CC feerred to as ORFX proteins, professor of ORFX polymucleotides at least 85% identical to

the ORFX nucleic acid sequences, vectors and host cells comprising ORFX

DAN79587 represent of ORFX proteins, antibodies

CC pecific for ORFX proteins, methods of screening for modulators of ORFX expression or

activity, and methods of screening for modulators of ORFX expression or

activity, and methods of screening for modulators of ORFX expression or

CC promotion of ORFX proteins of the invention have a wide

CC promotion activity, and methods of screening individual for a predisposition to an

CC classe growth, angiogenesis, activity thrombolytic activity,

CC classe growth, angiogenesis, activity thrombolytic activity,

CC classe growth, angiogenesis, activity thrombolytic activity,

CC classe growth, and mitinflammatory activity, thrombolytic activity,

CC companied that activity, and may also be involved in the determination

CC bodily characteristics, fertility and behaviour. ORFX proteins

CC bodily characteristics, fertility and behaviour. ORFX proteins

CC bodily characteristics, fertility and behaviour, of cancers,

CC bodily characteristics, fertility and behaviour, of cancers,

CC cardiovascular diseases, immune system disorders disease,

CC cardiovascular diseases, immune system disorders, disorders related to

CC cardiovascular diseases, immune system disorders, disorders related to

CC cardiovascular diseases, and infections diseases cancers of primers and probes, in the deterition, disorders such as a source of primers and probes, in the deterition and other parkogens. ORFX proteins may also be used as a

SOURCE of primers and probes, in the deterition of ORFX diagnosis, treatment and monitoring of ORFX-associated diseases Sequences ABP31028-ABP35561 represent 4534 novel human proteins

Sequence 309 BP; 91 A; 65 C; 68 G; 85 T; 0 U; 0 Other;

ö 740 800 120 860 920 240 980 GATCCTTATGCAAAGGCTTATGCAAAACTTACGTCACTTTTTGAGCAAAGAATGGACTCG 180 GATGTCACTATACTTACACCTAGTACCATCGCCATTGAGGCATTGCTAAAGATGGGAAGT 300 9 TATGCTAATGCTGATGCCAGAGTTTCACTTGAACATTTGCATTAAAACAAGGCCCATAAT GATGTCTCTAAGCTGACACCTACTGATATTGCAATTGAGTCACTTCATAAGATCGAGAGC 681 AACTGGAGATATATGAAGAGGGCCTATCTGTTTGGTTAGATGTGCCCTTGGATGCTCTT 1 AATTGGAGTTACATGAAGAAGGGCTGACCGTATGGTTAGATGTCCCACTGGATGCACTT GCAAGAAGAATTGCTGCTGTAGGAACCGCGTCTCGACCACTCTTGCATCAGGAATCCGGT TATGCAAATGCAGATGTAAGGGTTTCTCTGGAAGAGATTGCATGTAAACAAGGTCATGAT Gaps ö 13.1%; Score 157; DB 6; Length 309; 69.3%; Pred. No. 1.8e-26; 95; Indels Pred. No. 1.8e-0; Mismatches Query Match 13.1' Best Local Similarity 69.3 Matches 214; Conservative 981 TTCGTCATC 989 61 741 801 121 861 181 921 셤 ò g ò 셤 셤 g ઠે 8 ઠે δ

Novel genes that confer altered metabolic characteristics in Nicotiana benthamiana plants, useful for altering the levels of metabolites e.g. acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols. Plant DNA sequence which confers altered metabolic characteristic #5638. alcohol metabolism; fatty acid metabolism; branched fatty acid metabolism; alkaloid metabolism; amino acid metabolism; ester metabolism; glyceride metabolism; phenolic metabolism; carbohydrate metabolism; sterol metabolism; terpene metabolism; isoprenoid metabolism; ketone metabolism; alkyne metabolism; hydrocarbon metabolism; ketone metabolism; quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds. Pell RJ; r Miller BA; B, Mccreary DA, Pell RJ Shukla V, Larrinua I, metabolic characteristic; plant; acid metabolism; Blakeslee Reddy AS, BP. 31-AUG-2001; 2001US-0316471P. 30-AUG-2002; 2002WO-US027884. (DOWC) DOW CHEM CO. (DOWC) DOW AGROSCIENCES LLC. ADK58255 standard; DNA; 329 (first entry) מ' מ' 301 TTTCTTACC 309 Gachotte Crosley WPI; 2003-313091/30. WO2003020936-A1. Unidentified. 06-MAY-2004 13-MAR-2003. Oriedo JVB, Weglarz T, ADK58255; altered RESULT 12 ADK58255

The invention comprises DNA sequences which confer an altered metabolic characteristic when they are expressed in a plant. The DNA sequences of the invention are useful for producing plants with an altered metabolic characteristic, such as: altered acid metabolism, alcohol metabolism, fatty acid metabolism, alcohol metabolism, altered acid metabolism, altered ester metabolism, altered amino acid metabolism, altered ester metabolism, altered anion acid metabolism altered ester metabolism, altered sterol, oxygenated terpene, or isopremoid metabolism, altered sterol, oxygenated terpene, or isopremoid metabolism, altered sterol. sexual PCR procedures. The present nucleic acid represents a metabolism, ketone or quinone metabolism. The DNA sequences of the invention may be used to provide disease resistance in a plant and DNA sequence of the invention. shuffling or

Claim 1; SEQ ID NO 5638; 2576pp; English.

Sequence 329 BP; 93 A; 52 C; 88 G; 96 T; 0 U; 0 Other;

ö 412 ACTTGAACGGGAGGTGTATTTACCTAGTAGGAATGATGGCTTCTGGAAAAGTACTGTGG 0; Gaps Score 138.4; DB 10; Length 329; Pred. No. 3.7e-22; 0; Mismatches 111; Indels 0; 11.5%; 64.9%; Matches 205; Conservative Similarity Query Match Local 8 531 472 GGAAGATTATGTCTGAAGTCTTGGGTTATTCGTTCTTTGATAGTGACAAGTTAGTGGAGC

14 ATTTGAATGGACGATCTATGTACCTTGTCGGAATGATGGGTTCTGGGGAAAACAACTGTGG 73

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ADR60835 standard; cDNA; 1010
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                                                                            651
                                                                                                                                                Cotton; plant; EST; expressed sequence tag; transgenic plant; androecium; variety Nocotton33B; library L18382B; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; cissue printing; ss.
134 AGGCGATGAATGGAACTTCTGTTGCAGAGATATTTGTTCATCACGGAGAATTTTTTA 193
                                                                                                    GAGGAÁAGGÁGÁCCGATGCGCTTAAGAAGCTCTCTTCGAGGTATCAAGTTGTTGTTTCCA 253
                                                                                                                              CCGGAGGTGGTGTTATCCGACCAATTAACTGGAGATATATGAAGAGGGGCCTATCTG 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to 17880 cotton expressed sequence tags (ESTs; ACN6520-ACN63099). The ESTs were isolated from cDNA libraries generated from primed or non-primed seeds from variety DPSOB, mature seeds from variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium tissue, developing fibres, carpel walls and septa from variety Nucotton33B. The invention also relates to substantially purified proteins or their fragments encoded by nucleic acid molecules of the invention, and to transformed plants having a nucleic acid construct comprising a nucleic acid of the invention. The cotton ESTs are useful as molecular tags to isolate genetic regions, to isolate genes, to map genes, to determine gene function and to determining whether genes are members of a particular gene function and to determining whether genes are used for isolating a variety of agronomically significant genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular
                         AAGCTGTTGGAATGCCATCAGTTGCCCAAATATTCAAGGTCCATAGTGAAGCCTTCTTTC
                                                                            GGGATAATGAGAGTAGTGTCTTGAGAGATTTGTCCTCCATGCGACGATTAGTTGTTGCCA
                                                                                                                                                                                                                                                                                                                                                      Cotton androecium tissue EST Clone ID: LIB3828-016-Q1-N6-D8, SEQ:7361.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 7361; 34pp; English.
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                                                                                                                                                                                                                                                                          ACN52580 standard; cDNA; 573 BP
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                                                                                                                                                                                  TTTGGTTAGATGTGCC
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FENG P C C.
FINCHER K L.
ZIEGLER T E.
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cassociated with plant growth, quality, yield, and could also serve as links in metabolic and catabolic pathways. The nucleic acid molecules are also useful for identifying genes important in initiating and maintaining seed germination or that may be used to mitigate stresses encountered during seed germination. The ESTs additionally enable the acquisition of promoters and cis-regulatory elements which will be useful to express agronomically significant genes in these tissues and/or other tissues, and also permits the acquisition of molecular markers useful in breeding schemes, genetic and molecular mapping, and in cloning of agronomically significant genes. The nucleic acid molecules are further useful for detecting the expression level or pattern of a protein or mRNA and for detecting the presence or quantity of a protein by tissue printing. The present sequence represents a specifically claimed EST isolated from a cotton variety Nucotton33B androedium tissue cDNA library (LIB3828). The sequence data for this patent did not form part of the printed conscious, but was obtained in electronic format directly from the US patent office at sequence.html?DocID=US20040123340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           333 craaagcaaargccagggrrrcarrgraagaaarrgcrggcaaacraggrraragagarg 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   688 GATATAT---GAAGAGGGCCTATCTGTTTGGTTAGATGTGCCCTTGGATGCTCTTGCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.3%; Score 135.2; DB 13; Length 573; 64.4%; Pred. No. 2.4e-21; ive 0; Mismatches 118; Indels 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 573 BP; 183 A; 138 C; 86 G; 166 T; 0 U; 0 Other;
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877 ACAAAGG-CITAAAACGICTGICITACCTTTIGGAACAGAGGGGTAAAAAATATGCTAAA 935
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                                                                                                                                                                                                                                                                                                               633 CGACGATTAGTTGCCACCGGAGGTGGTGCTGTTATCCGACCAATTAACTGGAGATAT
                                                                              697 AAACAACTIGITGITICIACTGGGGAGGTGCAGTTGTACAGGATGTGAACTGGGACTAT
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                                                                                                                                                             AT---GAAGAGGGCCTATCTGTTTGGTTAGATGTGCCCTTGGATGCTCTTGCTAGGCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   870 GCAGATGTAAGGGTTTCTCTGGAAGAGATTGCATGTAAACAAGGTC
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12-DEC-2001; 2001US-00021323.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a recombinant polymucleotide comprising any of the 58798 Cotton plant cDNA sequences mentioned in the specification.

Also a recombinant polypeptide comprising any of the 58798 amino acid sequences mentioned in the specification and producing a plant having an improved property.

Comprises transforming a plant with a recombinant construct comprising a promoter region functional in a plant cell operably joined to a sociated promoter region functional in a plant cell operably joined to a seciated polymucleotide comprising a coding sequence for a polypeptide associated with the property, and growing the transformed plant. The polypeptide is useful for improving plant cold tolerance, manipulating growth rate in plant cells by modification of the cell cycle pathway, improving plant councing galactomannan for lighin or plant growth regulators, improving plant tolerance to extreme osmortic conditions or peaks, improving plant tolerance to extreme osmortic conditions or to pathogens or peaks, improving plant companion in plants, improving plant tolerance to extreme osmortic conditions or to pathogens or peaks, improving yield by modification of photosynthesis, modifying seed oil or protein yield and/or content, improving yield by modification of carbohydrate, nitrogen or plant growth and development under at least one stress condition. The polymucleotide and polypeptide may also be used in recombinant DNA content content can are an lusic severame of constructs, in physical arrays of modecules, as plant breeding markers, constructs, in a plant promoter promoter.
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                                                                                                                                                                                                                                                                                                                                                                                                                         New recombinant nucleic acid molecules and polypeptides from Gossypium hirsutum, useful for producing plants with improved biological characteristics (e.g. improved plant cold or drought tolerance).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTGACGAAGCTCTCCTGTTGAAGAGAAAATCAGAAGAAGTTCTGTTCTACTTGAACGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 1616; 14pp; English.
07-MAY-2001; 2001US-00849529.
12-DEC-2001; 2001US-00021323.
                                                                                                                                                                                                                                                                    Cao Y;
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useful for improving plant cold tolerance, manipulating growth rate in plant cells by modification of the cell cycle pathway, improving plant drought tolerance, providing increased resistance to plant disease.

producing galactomannan for lighth or plant growth regulators), improving plant tolerance, improving plant tolerance to herbicides, increasing the rate of homologous recombination in plants, improving plant tolerance to extreme osmotic conditions or to pathogens or pests, improving yield to extreme osmotic conditions or to pathogens or pests, improving yield and/or content, improving yield by modification of carbohydrate, nitrogen or phosphorus use and/or uptake, or improving yield by providing improved plant growth and development under at least one stress condition. The polymuclectide and polypeptide may also be used in recombinant DNA constructs, in physical arrays of modecules, as plant breeding markers, or in computer-based storage and analysis systems. The present sequence is a Cotton plant cDNA of the invention. NOTE: The sequence data for this patent did not forme directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TCTACTGGCGGAGGTGCACTGTACGGGATGTGGAACTAGGGACTATATGCAGAAGAAGAAGGGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       segdata uspto.gov/sequence.html?DocID=20040181830. However only 6585 polynucleotide sequences were available, the remaining 52213 polynucleotides and all 58798 protein sequences were not present.
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Matches 235, Conservative
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"Sequence 1, Application US/09073569; Sequence 1, Application US/09073569; Patent No. 6084088; GENERAL INFORMATION: APPLICANT: Sheppard, Paul O.; APPLICANT: Grossmann, Angelika
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5350.224 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 15, A
                                                                                                                                                                                                                                                                   Description
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'cgn2 6/ptodata1/ina/6A_COMB.seq:*
'cgn2 6/ptodata1/ina/6B_COMB.seq:*
'cgn2 6/ptodata1/ina/6B_COMB.seq:*
'cgn2 6/ptodata1/ina/PCTUS COMB.seq:*
'cgn2 6/ptodata1/ina/PCTUS COMB.seq:*
5.1.6
Compugen Ltd.
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US-08-708-123D-3
US-08-563-153A-3
US-08-570-142D-3
US-09-638-524B-3
US-09-147-2198-2
US-09-127-2198-2
US-09-127-2198-2
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-09-621-976-18068
-09-621-976-18054
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-09-621-976-18058
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US-08-481-190-15
PCT-US93-00869-15
                                                                                                                                                                                                                                                                                                                                                                                                                   Total number of hits satisfying chosen parameters
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-651-136C-7
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version :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                                                                   nucleic search, using sw model
                                                                                                                                                                                                                                                                                                           IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
GenCore (c) 1993 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq length: 0
seq length: 200000000
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1200
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Match
                                                                                                                                                                                                                     Title:
Perfect score:
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                                                                                     nucleic
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Maximum i
                                                                                                                               Run on:
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Sequence 2023, Application US/09328352

Batent NO. 6522958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 2023
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                                                                                                                                                                                   8, Appli
1, Appli
18066, A
80, Appl
                                                                                                                                                                                                                                                                                                                  15134, A
9, Appli
1, Appli
35, Appl
13076, A
5, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    548 ATCAGTTGCCCAAATATTCAAGGTCCATAGTGAAGCCTTCTTTCGGGATAATGAGAGTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACTATICCCIGGATTITIGAAAAGAAGGAGAAGTCGGCTTCCGTACGCGTGAACTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGTCTTGGGTTATTCGTTCTTTGATAGTGACAAGTTAGTGGAGCAAGCTGTTGGAATGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACTATTAGGGCGTGAATTTTAGATAGTGATCATGAAATTGAGCGCAAGACAGG----GGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        608 TGTCTTGAGAGATTTGTCCTCCATGCGACGATTAGTTGTTGCCACCGGAGGTGGTGCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATTTACCTAGTAGGAATGATGGGTTCTGGAAAAGTACTGTGGGGAAGATTATGTCTGA
                                                                                                         Sequence 1
Sequence 1
Sequence 1
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Sequence
Sequence
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Sequence
Sequence
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Pred. No. 0.00012;
0; Mismatches 125; Indels
US-09-713-550-10
US-09-825-294-10
US-09-970-966-10
US-07-861-458C-4
US-08-603-919-1
US-08-603-919-1
US-09-911-361-19
US-09-910-351-18
US-09-90-955C-8
US-09-621-976-18066
US-09-621-976-18134
US-09-621-976-15134
US-09-621-976-15134
US-09-621-976-15134
US-09-621-976-15134
US-09-940-16-13076
US-09-940-016-13076
US-09-940-016-13076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-2023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.6%;
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Best Local Similarity 52.8
Matches 143; Conservative
     US-09-328-352-2023
     93
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TATCCGACCAATTAACTGGAGATATATGAAG TACTCAGGCGCCTAATCGGGAGTTTTTAAAG

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COPOLOGY:
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4.5%; Score 53.8; DB 3; Length 1733;
Best Local Similarity 75.3%; Pred. No. 0.00045;
Matches 67; Conservative 0; Mismatches 22; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           No. 6001639el Endoglucanases
109
                                                                                                                                                                                              MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/073,569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1172 AAAAAAAAAAAAAAAAAAAAAAAA 1200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1621 AAAAAAAAAAAAAAAAAAAAAAAAAA 1649
TITLE OF INVENTION: NOVEL TUMOR ANTIGENS NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
                            STREET: 1201 Eastlake Avenue East CITY: Seattle STATE: WA
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/US/US/US/SUS/
FILING DATE:
PRIOR APPLICATION:
APPLICATION WHERE:
FILING DATE:
ATTONEY/AGENT INFORMATION:
NAME: Sawielak, Deborah A
REGISTRATION NUMBER: 37,438
REGISTRATION NUMBER: 97-14
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08651136C Patent No. 6001639 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schulein, Martin
Andersen, Lene N.
Lassen, Soren F.
Kauppinen, Markus S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lange, Lene
APPLICANT: Noilsen, Ruby I.
APPLICANT: Intera, Michiko
APPLICANT: Takagi, Shinobu
TITLE OF INVENTION: No. 60016.
NUMBER OF SEQUENCES: 109
CORRESPENDE: No. 60016390 No.
STREET: 405 Lexington Avenu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear FEATURE:
NAME/KEY: Coding Sequence LOCATION: 34...1344
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1733 Base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 206-442-6678
                                                                                                                                     COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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APPLICANT:
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Kauppinen, Markus S.
Lange, Lene
Nielsen, Ruby I.
Ihara, Michiko
THTLE OF INVENTION: No. 6387690el Endoglucanases
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6387690o No. 6387690disk of No. 6387690th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1025 ATATAGTCTTCCGAGTACATACTATTGAATGAAATAAGAGCGGCTCGGACCATGAGCAG 1084
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COUNTRY: United States of America
LIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
COMPUTER: BW PC COMpatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/229,911A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40; Indels
STATE: New TOLK
COMPUTER, TUT14-6401
COMPUTER READABLE FORM:
MEDIUW TYPE: FORM:
MEDIUW TYPE: FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/651,136C
FILING DATE: 21-MAX-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRICATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 33,728
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 7:
SEQUENCE CRARACTERISTICS:
LENGTH: 1154 Dase Pairs
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Pred, No. 0.00059;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Schulein, Martin
Andersen, Lene N.
Lassen, Soren F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 65.8
Matches 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: CDNA
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; LOCATION: 51..
US-08-651-136C-7
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 4.4%; Score 53; DB 3; Length 1154; Best Local Similarity 65.8%; Pred. No. 0.00059; Matches 77; Conservative 0; Mismatches 40; Indels
                                                       APPLICATION UNMER: 08/651,136
FILING DATE: 21-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4366.200-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEPHONE: 212-867-9655
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
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Sequence 15, Application US/08481190

Patent No. 6160204

GENERAL INFORMATION:
TITLE OF INVEXTION:
TITLE OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yahwak & Associates
STREET: 25 SKytop Drive
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 203,533
FILING DATE: 02-24-1994
ATTONNEY, AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
REFERENCE/DOCKET NUMBER: US 824
REFERENCE/DOCKET NUMBER: US 816 CIP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION: 51..935
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-229-911A-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,190
FILING DATE: 13-Jan-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                               LENGTH: 1154 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (203) 268-1951
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: CDNA PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
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1105 TTTGTAAAGGAATGGAAGAAGGGAGCTAATAATCCGAAGTGTGCCGTTGGCTGAAAAAA 1164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 TIGITAATGCTATGTATGAATAAATAAATGGTTGTCTTCCATTTAATTTTTAAAA 181
                                                                                                                                                                                                                                                                            1105 TTTGTAAAGGAATGGAAGAAGAGGAGCTAATAATCCGAAGTGTGCCGTTGGCTGAAAAAA
                                                                                                                                                                                                                            Gaps
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4.4%; Score 52.8; DB 5; Length 2;
Best Local Similarity 71.9%; Pred. No. 0.00028;
Matches 69; Conservative 0; Mismatches 27; Indels
                                                                                                                                                                                                                            27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 15, Application PC/TUS9300869
Sequence 15, Application PC/TUS9300869
GENERAL INFORMATION:
APPLICANT: John C. Steffens
TITLE OF INVENTION: Polyphenol Oxidase cDNAs: Cloning
TITLE OF INVENTION: and Applications
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Yahwak & Associates
STREET: 25 SKYCOP Drive
                                                                                                                                                                                                                                                                                                                                                                             1165 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 1200
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Pred. No. 0.00028;
                                                                                                                                                                          Query Match
4.4%; Score 52.8; Di
Best Local Similarity 71.9%; Pred. No. 0.000
Matches 69; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: CORNECTIONE
COUNTRY: USA
ZIP: 06611
COMPUTER READABLE PORM:
MEDIUM TYPE: floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/00869
FILING DATE: 19930129
FILING DATE: 19930129
ATTORNEY/AGENT INPORMATION:
NAME: George M. Yahwak
REJISTRATION NUMBER: 26,824
REFERENCE/DOCKET NUMBER: 26,824
REFERENCE/DOCKET NUMBER: CRF D-1057
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
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INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 base pairs
; LENGTH: 222 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-481-190-15
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STATE: Connecticut
COUNTRY: USA
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86.6%; Pred. No. 0.00081;
tive 0; Mismatches 9; Indels 0
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APPLICANT: Allen, Stephen M.
APPLICANT: Falco, Carl S.
APPLICANT: Tarczynski, Mitchell
TITLE OF INVENTION: Serine O-Acetyltransferase;
FILE REPERENCE: BB1514
CURRENT APPLICATION NUMBER: US/10/151,832
CURRENT FILING DATE: 2002-05-21
FRIOR APPLICATION NUMBER: 60/292,411
FRIOR APPLICATION NUMBER: 60/292,411
FRIOR FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Microsoft Office 97
LENGTH: 1308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 27, Application US/09443041A
Fatent No. 6465717
GENERAL INFORMATION:
APPLICANT: Famodu, Omolayo O.
APPLICANT: Rafalski, Antoni
APPLICANT: Rafalski, Antoni
APPLICANT: Shen, Jennia
TITLE OF INVENTION: Sterol Metabolism Enzymes
FILE REFERENCE:
CURRENT FILING DATE: 1999-11-18
PRIOR FILING DATE: 1998-11-20
              Sequence 1, Application US/10151832
Patent No. 6831206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 33
SOFTWARE: Microsoft Office 97
SEQ ID NO 27
LENGTH: 1447
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Matches 58; Conservative
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CORGANISM: Glycine max
US-09-443-041A-27
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Matches 70; Conserv
                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Zea mays
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US-10-151-832-1
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RESULT 9

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1102 TTATTTGTAAAGGAATGGAAGAAGAAGGGGGCTAATAATCCGAAGTGTGCCGTTGGCTGAAAA 1161
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GENERAL INFORMATION:

APPLICANT: Tartaglia, Louis A.

APPLICANT: Tapper, Robert I.

APPLICANT: Culpepper, Janice A.

APPLICANT: Culpepper, Janice A.

TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT

TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.

STREET: 225 Pranklin Street
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                                                                                                  APPLICANT: Rosen et al.
TITLE OF INVENTION: 28 Human Secreted Proteins
FILE REFERENCE: PZ003P1.US
                                                                                                                                                                                 TILE KEKEKENIE PZUGJEL.US

CURRENT PELING DATE: 1998-09-11

EARLIER APPLICATION NUMBER: US/09/152,060

CURRENT FILING DATE: 1998-09-11

EARLIER PELING DATE: 1998-03-12

EARLIER PELING DATE: 1998-03-14

EARLIER PELING DATE: 1997-03-14

EARLIER PILING DATE: 1997-03-14

EARLIER PELING DATE: 1997-03-14

EARLIER PELING DATE: 1997-03-14

EARLIER PELING DATE: 1997-03-16

EARLIER PELING DATE: 1997-05-30

EARLIER FILING DATE: 1997-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (2041)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-152-060-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (2040)
OTHER INFORMATION: n equals a,t,g, or c
Sequence 22, Application US/09152060 Patent No. 6448230 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 118
SOFTWARE: Patentin Ver. 2.0
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Matches 70; Conserv
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1086 ATAGAGCATCGTTGAGTTATTGTAAAGGAATGGAAGAAGGGAGCTAATAATCCGAAGTG 1145
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Sequence 3, Application US/09137132
Patent No. 6380363
CENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
APPLICANT: White, David W.
TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3744 ATAGATTATAGTTGTGGGTGGGAGAGAAAAGAAACCAGAGTCCAAATTTGAAAATAAT 3803
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66.1%; Pred. No. 0.0014;
tive 0; Mismatches 39; Indels 0
                                                                                   MEDIUM TYRE: LABACTERE COMPUTER: LBM COMPAGE LDE COMPUTER: LBM COMPAGE LDE COMPUTER: LBM COMPAGE LDE COMPUTER: LBM COMPAGE LDE COPERATING SYSTEM: Windows95 SOFTWARE: FaceSEG for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/64,564 FILING DATE: 28-MAY-1997 APPLICATION NUMBER: US 08/64,564 FILING DATE: 28-MAY-1997 APPLICATION NUMBER: US 08/59,455 FILING DATE: 2-JAN-1996 APPLICATION NUMBER: US 08/59,455 FILING DATE: 2-JAN-1996 APPLICATION NUMBER: US 08/59,455 FILING DATE: 28-DEC-1995 APPLICATION NUMBER: US 08/59,465 FILING DATE: 18-DEC-1995 APPLICATION NUMBER: US 08/56,622 APPLICATION NUMBER: US 08/56,633 FILING DATE: 04-DEC-1995 APPLICATION NUMBER: US 08/56,633 FILING DATE: O4-DEC-1995 APPLICATION UNFORWAITON:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (617) 542-5070
(617) 542-8906
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INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 3871 base pairs
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Best Local Similarity 66.1
Matches 76; Conservative
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STRANDEDNESS: double
TOPOLOGY: unknown
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      194...3688
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US-09-137-132-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                  CURRENT TITE: IBM COMPAGINE
COMPUTER: IBM COMPAGINE
CORFURATING SYSTEM: Windows95
SOFTWARE: FASESO for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,455B
FILING DATE: 22-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/56,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/56,622
FILING DATE: 27-NOV-1995
APPLICATION NUMBER: 08/56,63
FILING DATE: 27-NOV-1995
APPLICATION NUMBER: 08/56,63
FILING DATE: 27-NOV-1995
APPLICATION NUMBER: 35,283
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 35,283
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09069781B
Patent No. 6287782
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tapper, Robert I.
APPLICANT: Tapper, Robert I.
APPLICANT: Tapper, Tartaglia, Louis A.
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tartaglia, Louis A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE DIAGNOSIS AND TITLE OF INVENTION: INCLUDING OBESITY A.
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 200154
INPORMATION POR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 3871 base pairs TYPE: nucleic acid STRANDENRSS: double TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Coding Sequence
LOCATION: 194...3688
                           ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown MOLECULE TYPE: CDNA FEATURE:
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LOCATION:
US-08-599-455B-3
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Matches
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REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Coding Sequence LOCATION: 194...3688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3871 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     617-542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: unknown MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                   Boston
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US-08-864-564A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1086 ATAGAGCATCGTTGAGTTATTTGTAAAGGAATGGAAGAGGGAGCTAATAATCCGAAGTG 1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3744 ATAGATTATAGTTGTGGGGGGGGAGAGAAAGAAACCAGAGTCCAAATTTGAAAATAAT 3803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 52.6; DB 3; Length 3871;
Pred. No. 0.0014;
0; Mismatches 39; Indels 0
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
                                                                                                                                                                                                                                       MEDIUM TYPE: UISKELLE
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/137,132
FILING DATE: 18-AUG-1998
PRIOR APPLICATION NUMBER: 08/764,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: 08/768,123
FILING DATE: 26-ARP-1996
APPLICATION NUMBER: 08/539,455
FILING DATE: 26-ARP-1996
APPLICATION NUMBER: 08/539,455
FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/59,455
FILING DATE: 21-DEC-1995
APPLICATION NUMBER: 08/56,485
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/56,485
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/56,662
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/56,662
FILING DATE: 27-NOV-1995
APPLICATION NUMBER: 08/56,663
FILING DATE: 37-NOV-1995
APPLICATION NUMBER: 08/56,663
APPLICATION NUMBER: 08/56,663
FILING DATE: 37-NOV-1995
ATTOMEVACATION NUMBER: 08/56,663
ATTOMEVACATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/019004
TELERAX: 617-542-5070
                   NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson,
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3871 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 66.1#
Matches 76; Conservative
                                                                                                                                                                              ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: unknown MOLECULE TYPE: CDNA
                                                                                                                 Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY:
; LOCATION:
US-09-137-132-3
                                                                                                                                                                  COUNTRY:
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US-08-864-564A-3; Sequence 3, Application US/08864564A; Patent No. 6395498

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3744 ATAGATTATAGATGGGGGGGGAGAAAAGAAAGCAGAGTCCAAATTGAAAATA 3803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Fish & Richardson, P.C. 225 Franklin Street
                                                                                                                                                                                                                                  Sequence 3, Application US/08708123D Patent No. 6482927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 0733
TELECOMUNICATION INPORMATION:
TELEPHONE: 617-542-8906
TELEFAX: 617-542-8906
TELEX: 200154 542-8906
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3871 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Coding Sequence
LOCATION: 194...3688
US-08-708-123D-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: unknown MOLECULE TYPE: CDNA FEATURE:
                                                                                                                                                                                                                                                                               GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boston
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STRANDEDNESS:
                                                                                                                                                                                      RESULT 15
US-08-708-123D-3
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                                                                                                                                    APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Olipepper, Janice A.
APPLICANT: White, David W.
TITLE OP INVENTION: THE OB RECEPTOR AND METHODS FOR
TITLE OP INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
TITLE OP INVENTION: INCLUDING OBESITY AND CACHEXIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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4.4%; Score 52.6; DB 3; Length 3871;
Best Local Similarity 66.1%; Pred. No. 0.0014;
Matches 76; Conservative 0; Mismatches 39; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: US
ZIP: 02110-2804
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/094,410
TIING DATE: OP-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07334/019003
                                                                                                                                                                                                                                                                                                                                                Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 09-JUN-1978

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/64,564

FILING DATE: 28-MAY-1997
APPLICATION NUMBER: 08/708,123

FILING DATE: 03-SEP-1996
APPLICATION NUMBER: 08/599,455

FILING DATE: 26-APR-1996
APPLICATION NUMBER: 08/599,455

FILING DATE: 22-JAN-1996
APPLICATION NUMBER: 08/599,455

FILING DATE: 28-DEC-1995
APPLICATION NUMBER: 08/599,455

FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/509,142

FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/569,485

FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/569,485

FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622

FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622

FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Meiklejohn, Ph.D., Anita L. REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-6970
                                                                     Sequence 3, Application US/09094410
                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardso
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 3971 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coding Sequence 194...3688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown MOLECULE TYPE: CDNA
                                                                                           Patent No. 6403552
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY:
; LOCATION:
US-09-094-410-3
                                        US-09-094-410-3
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APPLICANT: Tartaglia, Louis A.
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Culpepper, Janice A.
APPLICANT: Culpepper, Janice A.
APPLICANT: White, David W.
TITLE OF INVENTION: THE DIAGNOSIS AND METHODS FOR
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS,
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
4.4%; Score 52.6; DB 4; Length 3871; 66.1%; Pred. No. 0.0014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER DISKETTE

COMPUTER: DISKETTE

COMPUTER: IBM Compatible

COMPUTER: IBM Compatible

CORPUTARE: FastSED for Windows Version 2.0

SOFTWARE: FastSED for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/68/123D

FILING DATE: 26-APR-1996

APPLICATION NUMBER: 08/599,455

FILING DATE: 22-JAN-1996

APPLICATION NUMBER: 08/599,153

FILING DATE: 28-DEC-1995

APPLICATION NUMBER: 08/569,485

FILING DATE: 1-DEC-1995

APPLICATION NUMBER: 08/56,622

FILING DATE: 04-DEC-1995

APPLICATION NUMBER: 08/56,63

FILING DATE: 37-NOV-1995

ATCHARRY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,281

REGISTRATION NUMBER: 35,281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07334/019001
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Best Local Similarity
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0; Gaps	CGAAGTG	AATAAT	AA 1200	AA 3858
0;	\TC	g	3-	-3
39; Indels	GGAGCTAATA	BAGTCCAAATT	AAAAAAAAA	VAAAAAAAAA
39;	SAAC -	Ş	AA.	=₹
6.1	AA-	=₹	AA.	=
0; Mismatches	GTAAAGGAATGGAAGAGGG	AGAGAGAAAGA		AAAAAAAAA
·;	TTT	ဗ္ဗ	AA-	=₹
76; Conservative	1086 ATAGAGCATCGTTGAGTTATTTGTAAAGGAATGGAAGAAGGGGAGCTAATAATCGAAGTG 1145	3744 ATAGATTATAGTGGGTGGGAGAGAAAAAAACAACAGAGTCCAAATTTGAAATAAT 3803	1146 TGCCGTTGGCTGAAAAAAAAAAAAAAAAAAAAAAAAAAA	3804 TGTTCCCAACTGAAAAAAAAAAAAAAAAAAAAAAAAAAA
76;	4; – 9	- 4 - A	9 E-	-€ı
	108	374	114	380
Matches	ò	qq	ò	qq

Search completed: August 25, 2005, 20:28:31 Job time : 368 secs

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August 25, 2005, 17:26:08; Search time 888 Seconds (without alignments) 8842.013 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Applications NA:*

1: /cgn2 6/ptodata/1/pubpna/USO7 PUBCOMB.seq:*
2: /cgn2 6/ptodata/1/pubpna/PCT NEW PUB.seq:*
3: /cgn2 6/ptodata/1/pubpna/USO6 NEW PUB.seq:*
4: /cgn2 6/ptodata/1/pubpna/USO6 PUBCOMB.seq:*
5: /cgn2 6/ptodata/1/pubpna/USO6 PUBCOMB.seq:*
7: /cgn2 6/ptodata/1/pubpna/USO8 NEW PUB.seq:*
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11: /cgn2 6/ptodata/1/pubpna/USO8 NEW PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7331713 segs, 3271544945 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                         OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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1200
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Database
                                                                                                                                                                                                                                           Run on:
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Description	Sequence 9, Appli	Sequence 30672, A	Sequence 16472, A			Sequence 31574, A	Sequence 13420, A
SUMMARIES	US-10-660-226-9	US-10-425-114-30672	US-10-425-115-16472	US-10-425-114-35273	US-10-425-115-16474	US-10-425-114-31574	US-10-767-701-13420
DB		18	20	18	20	18	19
% Query Match Length DB ID	1200	1059	1474	1228	1583	1241	1273
* Query Match	100.0	87.1	82.3	70.5	70.3	70.2	67.1
Score	1200	1045.4	988.2	846.2	843.4	841.8	802
Result No.	7	7	٣	4	ហ	9	7

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Gaps

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Query Match
100.0%; Score 1200;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1200; Conservative 0; Mismatches

TYPE: DNA CRGANISM: Zea mays US-10-660-226-9 LENGTH: 1200

DB 18; Length 1200; Indels

	œ	737.4	61.	m	20	S-1	equence	4
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	20	~	27.	4	20	4	Sequence 1680, Ap	ıΩ
	21	293	24.	σ	13	7	Sequence 84944, P	٨
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	24	241.6	20:	35	8 5	٠,	Sequence 70058, A	∢,
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	50	206.2	17.	36	20	-10-425-115-15155	Sequence 151552.	1,
υ	m	193.2	16.	œ	20	٠.	Sequence 162636,	
	31	193	16.	m	20	-10-739-930-523	Sequence 523, App	Ω
	32	191	15.	9	18	7	Sequence 137299,	,
	33	191	15.	9	18	ᅻ	Sequence 29612, A	K
	34	190.4	15.	N	18	∹	Sequence 18884, A	Ø
	32	٦,	13.	w.	77	-10-487-901-5640	Sequence 5640, Ap	Q,
	36	162.2	13.	0	200	∹'	Sequence 158029,	
	37	٦,	. 13	0	[]	o,	Sequence 8601, Ap	Ω
,	m c	2,4		ם ת	13	-10-437-963-2317	Sequence 2317, Ap	Q,
O		9.		67	20	٠,	Sequence 145002,	
	2 F	141.4	11.8	1096	8 0	-10-424-599-1136	Sequence 11365, A	∢-
	4.1	ה ה ה	: _	32	3 5	75	Sequence 21, Appl	٦ ډ
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ט	4	35	-	7	13	S-10-021-323-7361	Sequence 7361, Ap	. α
	45	31	ö	m	20	-10-425-115-334	Sequence 33448, A	A
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- •	Publication	, 6	APPLICACION US/108802 No HS2004006484881	04006484	4831	9220		
	GENERAL	É	INFORMATION:		1			
	APPL	Ä.	Cahoon,	Rebecca	跖.			
•	APPL	APPLICANT:	Falco,	S. Carl				
•	APPL	APPLICANT:	Famodu, Layo O.	Layo O	٠,			
	APPL	TCANT:	Dendina	שפות				
- •-	TITL	TITLE OF INVEN	OF INVENTION:	Chorismat	끍	e Biosynthesis Enzymes		
••	FILE	REFERE	NCE: BB-1159	1159-C				
•••	CURRENT	ENT APP	CURRENT APPLICATION NUMBER:	NUMBER: U		US/10/660,226		
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	PRIOR	R FILIN	G DATE:	1999-07	-16			
	PRIOR	R APPLI		UMBER: 1	EARLIER	ER APPLICATION NUMBER:	60/093,611	
•-	PRIOR	R FILIN	FILING DATE: E	EARLIER	FIL	NG DATE: July 21, 199		
•-	NUMBER	o i		S: 28				
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                                                                      184 TCGGGAGCCTGAGAGTCGCTGACCCGGCGGGACCTGCGGTTGCCGTGCGGGTTCGCGGGT
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; Sequence 35273, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
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Publication No. US20040214272A1
Publication No. US20040214272A1
Publication No. US20040214272A1
APPLICANT: La Rosa, Thomas J.
APPLICANT: Exou, Yihua
APPLICANT: Zou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 16472
LENGTH: 1474
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                    GCTTGCACCAGCAAAGGGGTGATGCTTATGCAAATGCAGATGTAAGGGTTTCTCTGGAAGA
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 AGGTGGTGCTGTTATCCGACCAATTAACTGGAGATATATGAAGAGGGGCCTATCTGTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Clone ID: MRT4577_115020C.1
US-10-425-115-16472
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US-10-425-115-16472
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Sequence 16474, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Vinua
APPLICANT: Cao, Yinua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 16474
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88.0%; Pred. No. 3.6e-221;
iive 0; Mismatches 121;
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ORGANISM: Zea mays
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US-10-425-115-16474
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               APPLICANT: Zhou, Yihua APPLICANT: Kovalic, David K. APPLICANT: Tabaska Jack E APPLICANT: Tabaska Jack E APPLICANT: Tabaska and Uses Thereof for Plant Improvement TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313) B CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 35273

LENGTH: 1228
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US-10-425-114-35273
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Pred. No. 5.4e-222;
0; Mismatches 128;
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Best Local Similarity 87.5%;
Matches 951; Conservative
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ORGANISM: Zea mays
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Sequence 31574, Application No. US20040034888A1

Sublication No. US20040034888A1

Sublication No. US20040034888A1

APPLICANT: Liu, Jingdong

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 31574
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                                                                                              Gaps
                                                                                            8
                                                       Length 1241;
                                                                                            Indels
                                                     Score 841.8; DB 18;
Pred. No. 8.8e-221;
0; Mismatches 122;
; OTHER INFORMATION: Clone ID: UC-ZMFLB73191D05_FLI
US-10-425-114-31574
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Sequence 16473, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yougwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 16473
                                                                                                                                                                                                                                                                                                                                                      GCACACTCCTGATAATCCAGCTAGCGACTCGCAAGCTGAGGATCCAAAGGATACA 1104
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                                                                                                  AATGGCCTTTTCTAAGCTCAGCATGCTTGCACACACAAAGGGGTGATGCTTATGCAAATGC 871
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                     TATGAAGAAGGCCTATCTGTTTGGTTAGATGTGCCCTTGGATGCTCTTGCTAGGCGTAT
                                                                                                                                                                                    925 AGAIGTAAAGGGTTTCTCTAGAAGAGATTGCATCTAAGCAAGGTCACCATGATGTCTCTAA
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Pred. No. 3.9e-192;
0; Mismatches 26; Indels 1;
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Best Local Similarity 96.6%;
Matches 764; Conservative
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Publication No. US20040172684A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21 (53335)B
CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 13420
LENGTH: 1273
                                                                               1043
                                        TCGAGAGCTTCGTCATCGAGCACACTGCTGATAGTTCAGCTAGCGACGCGCAAGCTGAGT 1032
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924 GTCATGGCGATGTCTCTAAGCTGATGCCGACTGATATCGCAATTGAGTCACTTCATAAGA 983
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                                                                      984 TCGAGAGTTTCGTCATCGAGCAGCTGCTGATAATCCAGCTAGCGACTCGCAAGCTGAGT
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US-10-767-701-13420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 67.1%; Score 805; DB 19; Best Local Similarity 87.6%; Pred. No. 1.2e-210; Matches 921; Conservative 0; Mismatches 110;
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US-10-767-701-13420
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                                                                                                                                                                       TGACCCGGGGGACCTGCGGTGTGCGGGCTCGCGGGTCCAAGCCCGTCGCACCGCT 310
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                                                 Gaps
                                                 24;
                         Length 1410;
                                                0; Mismatches 155; Indels
                         DB 19;
                         Score 660; DB 19
Pred. No. 1e-170;
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                         55.0%;
81.7%;
                        Query Match
Best Local Similarity 81.7
Matches 797; Conservative
   US-10-437-963-45320
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; Publication No. US20040123343A1
; GENERAL INFORMATION:
    APPLICANT: La Rosa, Thomas J.
    APPLICANT: Cao, Vinua
    APPLICANT: Cao, Vongwei
    APPLICANT: Buukharov, Andrey A.
    APPLICANT: Barbazuk, Brad
    APPLICANT: Barbazuk, Brad
    APPLICANT: Li, Ping
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    FILE REPERENCE: 38-21(3321)8
    CURRENT FILING DATE: 2003-05-14
    NUMBER OF SEQ ID NOS: 204966
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                                      GCCGCCGGCCTTCGGCTCCAGCCGGCACCGGCCGCCTACAGGCGCCCACCGGGAGCCT
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US-10-437-963-45320
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LENGTH: 1410
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TATTCAAGGTCCATAGTGAAGCCTTCTTTCGGGATAATGAGAGTAGTGTCTTGAGAGATT 621
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ORGANISM: Triticum aestivum
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Matches 606; Conservative
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                                                                                APPLICANT: Famodu, Layoto,
APPLICANT: Famodu, Layoto,
APPLICANT: Famodu, Layoto,
TITLE CANT: Rendina, Alan
TITLE OF INVENITION: Chorismate Biosynthesis Enzymes
FILE REPERENCE: B8-1159-C
CURRENT APPLICATION NUMBER: US/10/660,226
CURRENT FILING DATE: 2003-09-11
PRIOR PELING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: G0/093,611
PRIOR PLING DATE: EARLIER FILING DATE: July 21, 1998
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                 Length 1061;
                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                 Score 574; DB 18;
Pred. No. 4.1e-147;
0; Mismatches 145;
               Sequence 27, Application US/10660226
Publication No. US20040064848A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 81.5%;
Matches 693; Conservative
                                                                                                                                                                                                                                                                                                         ; ORGANISM: Triticum aestivum
US-10-660-226-27
                                                          APPLICANT: Cahoon, Rebecca
APPLICANT: Falco, S. Carl
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Sequence 4532, Application US/10739930

Publication No. US20040216190A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Kovalic, David K.

ATITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 4552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1007 TTCAGCTAGCGACGCGCAAGCTGAGTCGAGAGAAGATACAGACCTTGTAGAACCT 1066
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ACTCAGCATGCTCGCGGAGCGAAGGGGCGATGCTTATGCAAATGCTGATGTCAGAGTTTC
                                                                                                                                                                                                                                                                                           TATTGCTCTCGAGTCGCTCCACAAGATCGAGAGCTTTGTCGTCGAAGACACCGCT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----GTCGCCGACTCACAAACGGAATCGCAATCTCAAAGGATGCATACCTTGTAGGATAT
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30.8%; Score 370; DB 20; Length 1
Best Local Similarity 64.3%; Pred. No. 6.1e-91;
Matches 606; Conservative 0; Mismatches 325; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Clone ID: TRIAE-23APR03-CLUSTER25671_1
US-10-739-930-4532
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647

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837 GAGAAGGCTGTTGGTATTTCATCTGTTGCTGAGATCTTTCAGCTCCATAGCGAAACATTC 778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        708 TCTGTTTGGTTAGATGTGCCCTTGGATGCTCTTGCTAGGCGTATTGCTAAAGTGGGAACT 767
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                                                                                                                                             957 CCTTACTTGGATGGCCGTTGCGTTTATCTTGTAATGATGATGGGTTCAGGCAAAACTACA 898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCACCGGAGGTGGTGTTATCCGACCAATTAACTGGAGATATATGAAGAGGGCCTA 707
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          1017 AAGGTCCACTACTCTGCTGATGACGCTCTCATACTACAGCAAAAAGCCCAGGATGTTCTG 958
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Pred. No. 2.2e-89;
0; Mismatches 186; Indels
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US-10-660-226-25

§ Sequence 25, Application US/1066026

§ Publication No. US2004006484BA1

§ GENERAL INPORMATION:

§ APPLICANT: Cahoon, Rebecca E.

§ APPLICANT: Famedu, Layo O.

§ APPLICANT: Hitz, William D.

§ APPLICANT: Remedina, Alan

TITLE OF INVENTION: Chorismate Biosynthesis Enzymes

§ FILE REFERENCE: BB-1159-C.

© CURRENT FILING DATE: 2003-09-11

§ PRIOR APPLICATION NUMBER: US/10/660,226

CURRENT FILING DATE: 2003-09-11

§ PRIOR APPLICATION NUMBER: US/09/354,501

§ PRIOR PELLING DATE: EARLIER APPLICATION NUMBER: 60/

§ PRIOR PELLING DATE: EARLIER APPLICATION NUMBER: EARLIER EARLIER APPLICATION NUMBER: EARLIER EARLIER APPLICATION NUMBER: EARLIER ETLING DATE: JUJY 21, 1998
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Best Local Similarity 71.9%;
Matches 476; Conservative
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SOFTWARE: Microsoft Office 97
SEQ ID NO 25
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; ORGANISM: Triticum aestivum
US-10-660-226-25
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: APPLICANT: A Rosa, Thous APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: Bassociated With TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 68871
LENGTH: 1503
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TGTCCTCCATGCGACGATTAGTTGTTGCCACCGGAGGTGGTGCTGTTATCCGACCAATTA
                                                                                                                                                    ACTGGAGATATATGAAGAGGGCCTATCTGTTTGGTTAGATGTGCCCTTGGATGCTCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                             681 CGAAGCGCATTGCACAAGTTGGGACTGCTTCTCGGCCCCTTCTAGATCAGCCATCTGCTG
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30.6%; Score 367.8; DB 20; Length 1503;
Best Local Similarity 67.3%; Pred. No. 2.7e-90;
Matches 518; Conservative 0; Mismatches 252; Indels 0;
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US-10-425-115-68871
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US-10-425-115-68871/c
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CURRENT FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US/09/354,501
PRIOR FILING DATE: 1999-07-16
PRIOR PLICATION NUMBER: EABLIER APPLICATION NUMBER: 60/093,611
PRIOR FILING DATE: EARLIER FILING DATE: July 21, 1998
                                 Length 899
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US-10-660-226-19
Sequence 19, Application US/10660226
Publication No. US20040064848A1
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Falco, S. Carl
APPLICANT: Famodu, Layo O.
APPLICANT: Hitz, William D.
APPLICANT: Rendina, Alan
TITLE OF INVENTION: Chorismate Biosynthesis Enzymes
FILE REFERENCE: BB-1159-C.
                                 DB 18;
                                                                0; Mismatches 196;
                               Score 363.4; DB 1
Pred. No. 3.4e-89;
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Matches 481; Conservative
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Bublication No. US20040064848A1

GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Fancdu, Layo O.
APPLICANT: Fancdu, Layo O.
APPLICANT: Rendina, Alan
TITLE OF INVENTION: Chorismate Biosynthesis Enzymes
FILE REFERENCE: BB-1159-C
CURRENT APPLICATION NUMBER: US/10/660,226
CURRENT FILING DATE: 2003-09-11
PRIOR PILING DATE: 1999-07-16
PRIOR PLILING DATE: EARLIER FILING DATE: July 21, 1998
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 11
LENTH: 899
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ORGANISM: Zea mays
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                                                                                                          Score 362.6; DB 18; Length 960;
Pred. No. 5.8e-89;
0; Mismatches 189; Indels 0;
                                                                                                          Query Match 30.2%;
Best Local Similarity 71.6%;
Matches 476; Conservative
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 19
LENGTH: 960
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                                                     ; TYPE: DNA
; ORGANISM: Sorghum
US-10-660-226-19
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Submitted (25-ARR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA

If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.igr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnabbe, Iowa State, then clones may be requested from ZmDB:

www.zmdb.iastate.edu.
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2 (bases 1 to 1305)
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CA078453 SCRLAM100
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BQ577650 3524 1 39
CB684025 OSJNBÉ13C
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CA452817 RP3A-3 H0
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/dloaves word loaded to the growth medium to a final
concentration of 100 uM. Leaves were harvested and 27 hr
after treatment and pooled. Double-stranded cDNA was
cloned unidirectionally into different DraIII sites of the
pME185 FL3 vector (5-prime DraIII site is CACTGTGTG,
3-prime DraIII site is CACCATGTG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in the Human Genome Center, University of Tokyo Institute of Medical Science; plant material and RNA prepared at Texas A & M University; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude poly.
                                                                                                            01-APR-2004
                                                                                                                                                                                                                                                                                                                                                                     Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, P., Sullivan, R., Bradk, J., Bastman, A., Miller, V., Gonzalez, M., Antiuso, C., Chhabra, D., Johnson, H., Kamran, D. and Pratt, L.H. A. Sorghum EST database: mechanically damaged and methyl
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Sorghum.
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WOUNDI_48_G03.bl_A002 Wounded leaves Sorghum bicolor cDNA clone woundi_48_G03_A002 3', mRNA sequence.
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Outpublished (2003)
Other ESTs: WOUND1 48 G03.g1 A002
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 804;
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Pred. No. 4.7e-139;
0; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: Sug3-14 (TAGTCTAGCGGCCGCGACC)
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Sorghum bicolor"
/mol type="mRNA"
/cultivar="BTx623"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers
                                                                                                                                                                                                                                           Sorghum bicolor (sorghum)
Sorghum bicolor
                                                                                                                                                                                                  CN147205.1 GI:45987613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mmpratt@uga.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 88.5%;
Matches 700; Conservative
                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 804)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 706 542 1860
Fax: 706 583 0210
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SOURCE
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CN147205
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                                                                   CCTGCCTTCTCTCTCTTTTTTACACCTCACCTCCGGATCGCTCAGAGAGTCAG--AG
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  ed. No. 1.8e-188;
Mismatches 126;
  Pred.
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  87.48;
                      938; Conservative
Similarity
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/note="Organ: Apical meristem and tissues surrounding of mature plants; Vector: pSportl; Site_1: Sall; Site_2: NotI; An unidirectional cDNA library generated from [Apical meristem and tissues surrounding of mature plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             541 NGGTTTCTCTGGAAGAGTTGCATCTAAACAAGGCCACCATGATGTCTCTTAACTGACAC 600
                  Tel: 55 19 3788 1337
Fax: 55 19 3788 1039
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 007 row: D column: 04
Seg primer: T7 Promoter Primer.
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      Brazil
      SP,
                                                                                                                                                                                                                                                                                                                /clone lib="AM1"
/note="Organ: Apical meristem and
                                                                                                                                                                                               1. .667
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCRLAM1007D04"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 610.6; DB 6;
Pred. No. 7.8e-137;
0; Mismatches 35;
    Postal 6010, 13083-970, Campinas
                                                                                                                                                                               Location/Qualifiers
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nilarity 94.7%;
Conservative 0,
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Spermatophyta, Magnoliophyta, Lillopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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SCRLAM1007D04.g AM1 Saccharum officinarum cDNA clone SCRLAM1007D04
5', mRNA sequence.
CA078453
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Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda
The libraries that made SUCEST
Genet., Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
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BO577650 BS77650.1 GI:21480967
                                                                        310 TCCGACTCCGTGCGAAGAATCGTCCGGAGGTCATGAAAACTCGCACAACTCCGTTGACG
                                                                                                ----CTCCGTGCGAAGAAATCGTTCGGTGGTCATGAAAACTTGCATAACTCCGTTGACG
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Maize ESTs from various cDNA libraries sequenced
University
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Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Eax: 650 725 8221
Email: walbot@stanford.edu
Plate: 3524 1 39 1 row: F column: 07.
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/mol_type="MRNA"
/cultivar="B73"
/db_xref="taxon:4577"
/tissue type="mollen"
/dev stage="mature"
/lab_host="SOLR"
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//olone lib="RT2"
//oce="Organ: Root tips(0.3cm-long) from adult plants;
//octe="Organ: Root tips(0.3cm-long) from adult plants]. Not!! An unidirectional colva library generated from [Root tips(0.3cm-long) from adult plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitoyah). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"
                                                                                                                                                                                                   672 bp mRNA linear BST 24-SEP-2003
SCVPRT2077E07.g RT2 Saccharum officinarum cDNA clone SCVPRT2077E07
CA146167
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Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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Ciaxa Postal Genedia de Campinas
Caixa Postal Geno, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1139
Fax: 55 19 3788 1089
Email: parrudaequicamp.br
Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at http://www.bccenter.fcav.unesp.br
Plate: 077 row: E column: 07
Seq primer: 17 Pronocter Primer.
Location/Qualifiers
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Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P. The libraries that made SUCEST
Genet. Moll. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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/mol_type="mRNA"
/mol_type="mRNA"
/d_xref="taxon:4547"
/clone="SCVPRT2077E07"
/lab_host="DH10B"
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Pred. No. 2e-126;
0; Mismatches 36;
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Best Local Similarity 93.5
Matches 604; Conservative
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                                                                                                                                661 CAAATA 666
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                                                                                                                                                                                                                                                DEFINITION
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AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                       RESULT 4
CA146167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        214 ----CTCCGTGCCAAGAAATCGTCCGGAGGTCATGAAACATTGCATAACTCGGTTGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   270 AGCCCTCTTGCTAAAGAGAAAATCAGAAGAAGTTCTTCTTCTTTTAGAATGACGTGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96 cceccecaccececercraceccecesceseseseseseseseseseses de concecace de contra de contra
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                                                                                                          ΑZ
                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="Nipponbare"
                                                                                                          Box 210088, Tucson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:39947"
/clone="OSJNEf13C12"
/clone="CSJNEf13C12"
/dev stage="19 week"
/lab_host="DH10B"
/lone=lib="OSJNEfs"
/note="Vector: pBluescript II KS +;
Xhol; Uninfected Control"
                   Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Bo
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR PRimers
FORMARD: gta aaa cga cga cca gtg
                                                                                                                                                                                                                                                                                              BACKWARD: gga aac agc tat gac cat g
Plate: 13 row: C column: 12
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
  Unpublished (2003)
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Oryza sativa (japonica cultivar-group)
Bukaryota, Vizidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae, Oryza.

1 (bases 1 to 825)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
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OSJNEf13C12.f OSJNEf Oryza sativa (japonica cultivar-group) cDNA clone OSJNEf13C12 5', mRNA sequence.
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                /note="Vector: Stratagene's Uni-Zap XR (pBluescript SK-); Stete 1: BcoRI (5-prime); Site 2: XhoI (3-prime); Stete 2: ThoI (3-prime); Unamplified count library directionally cloned by Rima Kulikauskas using Stratagene's Uni-Zap system. Insert at Stees ranged from 0.5Kb to 2kb. 50 microliter aliquot had 318,000 pfu when it was made in Sept, 1995, from oligo dT-primed poly A+ RNA.
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Best Local Similarity 100.0%; Pred. No. 4.8e-126;
Matches 566; Conservative 0; Mismatches 0;
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Rp3A-3 HOI subtracted cDNA library of maize inbred line H95-Rp3A inoculated with Puccinia sorghi isolate INI Zea mays cDNA clone Rp3A-3 H01, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             361 AAAAAGTACTGTGGGGAAGATTATGTCTGAAGTCTTGGGTTATTCGTTCTTTGATAGTGA 420
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                                                                                                                                                                                                                                                                                                                        Query Match 45.8%; Score 549; DB 7; Length 549; Best Local Similarity 100.0%; Pred. No. 6.2e-122; Matches 549; Conservative 0; Mismatches 0; Indels
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//note="Organ: silks, husks, ears, pollen, shoot tips, leaf, root tips, whole seed, embryo; Vector: pCWV-SPORT 6-1; Site_1: EcoRV; Site_2: Not1; Maize Gene Discovery Project contracted with Invitrogen to produce a normalized, full length library in a pSport vector. This is a Gateway compatible vector, permitting clone movement to new vector backbones for expression in diverse host cells using recombination rather than restriction enzymes. Details of the Vector and sequencing primers are available at ZmDB in the BST library description tables. poly(A) + mRNA was prepared by Invitrogen, and equimolar amounts of RNA from each of the 12 tissue samples were mixed together for selection of mRNA with a 5' cap. After synthesis of CDNA, a normalization step was conducted against the mixture of RNA sources. This step effected a 20x to 80x reduction in common transcript types. Tissues prepared: 1. just emerging silks; 2. inner husks from ears of sample #1; 3. 20 dap aleurone; 4. immature tassels, stages from 1-2 mm to 1-2 cm; 5. 2 mm to 2 cm ears; 6. pollen; 7. 1 cm
                                                                                                                                                                                                                                                                                                                                                                                                                CO524949 State 1 CO6.y 1 3530 - Full length cDNA library created by Invitrogen from multiple tissues Zea mays cDNA, mRNA sequence.
                                                                                                                                                                            910
                                                                                                                                                                                                750 GGGCGAIGCTIAIGCAAAIGCTGAIGIGAGGGITICCTTGAAGAGAITGCAICTAAACA 809
                                                                                      ACCATCTGGTGATCCGTACGCAATGGCCTTTTCTAAGCTCAGCATGCTTGCACAGGAAG 850
                                                                                                                              690 ACCATCTGGTGATCCATACACAATGGCTTTTTCTAAACTCAGCATGCTCGCGGAGCAAAG 749
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1 (bases 1 to 549)
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                                                                                                                                                                     GGGTGATGCTTATGCAAATGCAGATGTAAGGGTTTCTCTGGAAGAGATTGCATGTAAACA
GGATGCTCTTGCTAGGCGTATTGCTAAAGTGGGAACTGCCTCTCCGTCCTTCTGGACCA
                           630 GGACGCTCTTGCTAGGGTATTGCTANAGTGGGGACTGCCTCCCGTCCTCTTCTAGATCA
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Maize ESTs from various cDNA libraries sequenced at Stanford
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Fax: 650 725 8221

Email: walboct@stanford.edu
Plate: 3530 1 165 1 row: C column: 06.
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/ organism="Zea mays"
/ orlitype="mRNA"
/ cultype="mRNA"
/ db_xref="taxon:4577"
/ tisuue_type="multiple"
/ dev stage="varies by tissue"
/ lab_host="DH10B"
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Unpublished (1999)
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vegetative shoot tips from 15 day old seedlings; all leaves with an expanded or partially expanded sheath were removed; 8. mature leaf tissue; 9. 0.5 cm long root tips from 15 day old seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and embryo; 12. 17 dap endosperm and embryo; 12. 17 dap endosperm and embryo. All of the sequenced clones in project 3530 will be archived at the University of Arizona along with the Unigene clones from the Maize Gene Discovery EST sequencing projects. Clones can be ordered through the ZmDB web site or directly from the University of Arizona (http://www.genome.arizona.edu/orders/). High density filters containing over 18,000 clones can also be ordered from the University of Arizona."

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217 120 277 180

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GCGGGCTCGCGGGTCCCAAGCCCGTCGCACTCCGACTCCGTGCGAAGAAATCGTCCGG 337 241 AGGTCATGAAAACTCGCACAACTCCGTTGACGAAGCTCTCCTGTTGAAGAAAAATCAGA 300 CGTCGGCCTGGCGCTGCAGGCGCGGCGGCGGCTTCGGCTTCCAGCCGGCACCGGGGCGG CCTACAGGCGCCCACCGGGAGCCTGAGAGTCGCTGACCCGGCGGGACCTGCGGTCGCTGT CCTACAGGCGCCCACCGGGAGCCTGAGAGTCGCTGACCCGGCGGGACCTGCGGTCGTTGT 1 ceacteerceccecercecreresecrececeseses AGAAGTTCTGTTCTACTTGAACGGGAGGTGTATTTACCTAGTAGGAATGATGGTTCTGG Gaps ; 0

240 397 457

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Zea mays Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD

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Oryza sativa (japonica cultivar-group)

SM Oryza sativa (japonica cultivar-group)

Eukaryota; viridiplancae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;

Ehrhartoidee; Oryzae; Oryza.

E (bases 1 to 833)

S Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,

Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.

Large-scale identification of ESTs involved in the interaction

between rice and Magnaporthe grisea

Unpublished (2003)

Contact: Rod Wing

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

85721-0088, USA
                                                                                                                                                                                                                                                                                                                  CB657302 833 bp mRNA linear EST 09-APR-2003 OSJNEC12117.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA clone OSJNEC12117 5', mRNA sequence.
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127 cceccesaecececreracecececesceaececececececeaeceaecereaecerece
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="GSNRC12117"
/tissue_type="Leaf"
/dev stage="3 week"
/lab_host="DH10B"
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Plate: 12 row: I column: 17
Seq primer: gta aaa cga ccg gtg.
Location/Qualifiers
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Fax: 520 621 9288
Email: http://genome.arizona.edu
PCR PRimers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="Rust-infected leaves"
/dev stage="4 week-old plants"
/clone_lib="subtracted cDNA library of maize inbred line
/clone_lib="subtracted cDNA library of maize inbred line
H95-Rp3A incoulated with Puccinia sorghi isolate INI"
/note="Vector: pUC19; Supression subtractive
hybridization; cloned into pUC19 vector. From a subtracted
cDNA library of maize inbred line H95 carrying the Rp3A
gene inoculated with an incompatible Puccinia sorghi
                                                                                               maize lines
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                                                                                                                                                                                                                   Department of Plant Pathology
Kansas State University
Kansas State University
Voly Throckmorton Plant Sciences Center, Manhattan, KS 66506, USA
Tel: 785-532-532
Fax: 785-532-5692
Email: jianfa@plantpath.ksu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          465 ACTGTGGGGAAGATTATGTCTGAAGTCTTGGGTTATTCGTTCTTTGATAGTGACAAGTTA
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                                1 (bases 1 to 619)
Bai,J., Fellers,J.P., Leach,J.E. and Hulbert,S.H.
Comparison of pathogen induced defense gene profiles
with different resistance genes
Contublished (2003)
Contact: Bai J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45.6%; Score 547.8; DB 6; 93.2%; Pred. No. 1.2e-121; Live 0; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Zea mays"
/mol_type="mRNA"
/strain="inbred line H95-Rp3A"
      clade; Panicoideae; Andropogoneae; Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4577"
/clone="Rp3A-3_H01"
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Matches 573;
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    (bases 1 to 620)

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                                                                                                                                    Length 609;
                                                                                                                                                                  Indels
                                                                                                                                    45.2%; Score 542; DB 2; I
larity 94.1%; Pred. No. 3.1e-120;
Conservative 0; Mismatches 30;
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Sorghum bicolor (sorghum)

Sorghum bicolor (sorghum)

Sorghum bicolor (sorghum)

Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae, Andropogoneae, Sorghum.

1 (bases 1 to 609)

Sordonnier-Pratt, M.-M., Gingle, A., Marsala, C. and Pratt, L.H.

An EST database from Sorghum: light-grown seedlings

Unpublished (2000)

Contact: Cordonnier-Pratt MM

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Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

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Pax: 106 583 0210
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LG1 353_A11.b1_A002 Light Grown 1 (LG1) Sorghum bicolor CDNA, mRNA
sequence.
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                               AGCTCTCCTGTTGAAGAGAAAATCAGAAGAGTTCTGTTCTACTTGAACGGGAGGTGTAT
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/mol_type="mRNA"
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High quality sequence stop:
POLYA=No.
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                                                  93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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                                                                                                                                                                                              /organism="Zea mays"
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/clone_lib="QCF"
                                                                                                                                                                                                                                                                                                                                                             45.1%; Score 540.8; DB 6; ilarity 92.4%; Pred. No. 6e-120; Conservative 0; Mismatches 47;
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 Unpublished (2003)
Contact: Genoplante
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CF636791 814 bp mRNA linear EST 02-OCT-2003 zmrww00_0B10-012-g04.83 zmrww00 Zea may8 cDNA 3', mRNA sequence.

CF636791/c LOCUS DEFINITION

us-10-660-226-9.rst

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/ organism="Saccharum officinarum"
/mol type="mRNA"
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/clone=lib="HR1"

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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
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SCJFHRICO8D05.9 HR1 Saccharum officinarum cDNA clone SCJFHR1CO8D05
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Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
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Universidade Estadual de Campinas
Gaixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
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44.2%; Score 530.8; DB 6;
Best Local Similarity 93.0%; Pred. No. 1.6e-117;
Matches 569; Conservative 0; Mismatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: parruda@unicamp.br
Clone distribution: clone distribution
through the Brazilian Clone Collection
http://www.bcccenter.fcav.unesp.br
Plate: COB row: D column: 05
Seg primer: T7 Promoter Primer.
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PCR. Plasmid DNA from the primary libraries then was converted to single-stranded circles and used as a temptate for PCR amplification using the T7 and T3 priming sites that flank the cloned cDNA inserts. The purified PCR products, representing the entire cDNA population cloned in each library, were used as a driver for normalization. Hybridization between the single-stranded library and the PCR products was carried out for 44 hours at 30c.

Non-hybridized single-stranded DNA circles were separated from hybridized single-stranded DNA circles were separated from hybridized DNA rendered partially double-stranded and electroporated into DHIOB. The total number of clones with insert was: zmrws05: 2.0x107; zmrws48: 4.2x107; zmrww00: 1.1x107. The background of empty clones was less than 2%. Insert size, determined by PCR of the entire library, ranged from 0.5kb to 2.5kb. (1) Sharp R E; Silk W K; Hsiao T C Growth of the Maize Primary Rock at Low Water Potentials I. Spatial Distribution of Expansive Growth. Plant Physiology (Rockville). 87(1). 1988: 50-57. (2) Spollen W G; LeNoble M E; Samuels T D; Bernstein N; Sharp R E. Abscisic acid accumulation maintains maize primary root elongation at low water potentials by restricting ethylene production. Plant Physiology (Rockville). 122(3). TAG TISGUE-ROCL_segment_3

TAG_SEQ_TCGCA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             012 CTAGCGACGCGCAAGCTGAGTCGCAGATCCAGAGATACAGACCTTGTAGAACCTTAATC 1071
266 CTAGCGACTCGCAAGCTGAGTCACAAGGATACATAATATCTTAATC 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               566 TTTGGTTAGATGTGCCCTTGGATGCTCTTGCTAGGCGTATTGCTAAAGTGGGAACCGCTT 507
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llarity 92.2%; Pred. No. 4.6e-119;
Conservative 0; Mismatches 48;
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                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                           Length 728;
                                                                                                                                                                                                                                                                                          Score 524; DB 7; Length 728
Pred. No. 7.2e-116;
0; Mismatches 75; Indels
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                                                                                                                                                                                                                                                                                        43.7%;
Best Local Similarity 87.1%;
Matches 603; Conservative
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatorophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum..

E 1 (bases 1 to 728)

Sorghum.

S Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C.,
Sun, F., Sullivan, R., Brady, J., Sastman, A., Miller, V., Gonzalez, M.,
Anfuso, C., Chhabra, D., Johnson, H., Kamran, D. and Pratt, L.H.
A Sorghum EST database: mechanically damaged and methyl
jamonate-traeted leaves
Unpublished (2003)
Other_ESTS: WOUNDI_23_C04.gl_A002
Contact: Cordonier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WOUND1_23_C04.bl_A002 Wounded leaves Sorghum bicolor cDNA clone CN144547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mmpratt@uga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science; plant material and RNA prepared at Texas A & M University,
Science; plant material and SNA prepared at Texas A & M University,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
Seq primer: Sug3-14 (TAGTCAGCGCCGCGACC)
     489
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                                                                                         TTTACTTAGTAGGAATGATGGGTTCTGGAAAAAGTACCGTGGGGAAGATATGTCTGAAG
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                                                                                                                                                                                                                                                                                             TCTTGGGTTATTCGTTCTTCGATAGTGACAAATTAGTGGAGGAAGCTGTTGGAATGCCTT
                                                                                                                                                                                                                                                                          TCTTGAGAGATTTGTCCTCCATGCGACGATTAGTTGTTGCCACCGGAGGTGGTGCTGTTA
                                                                      TTTACCTAGTAGGAATGATGGGTTCTGGAAAAGTACTGTGGGGAAGATTATGTCTGAAG
                                                                                                                                       TCTTGGGTTATTCGTTCTTTGATAGTGACAAGTTAGTGGAGCAAGCTGTTGGAATGCCAT
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The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Fax: 706 583 0210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Sorghum bicolor"
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/cultivar="BTx623"
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CN144547
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completed: August 25, 2005, 20:22:24
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                                                                                               Cryza sativa (japonica cultivar-group)

ENKaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzea; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryzeae; Oryzea; Cawara, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E., Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G. Laxge-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Balological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 621 9288
Email: http://genome.arizona.edu
PCR PRimers
FORWARD: gra aaa cga cgg cca gtg
RACKWARD: gra aaa cga cgg cca gtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1..818
//organism="Oryza sativa (japonica cultivar-group)"
//organism="MRNA"
/cultivar="Wipponbare"
/db_xref="taxon:39947"
/clone="OSYME13C12"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEf"
/clone_lib="OSJNEf"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2: XhoI; Uninfected Control"
CB684026 818 bp mRNA linear EST 09-APR-2003 OSJNEf13C12.r OSJNEf Oryza sativa (japonica cultivar-group) cDNA clone OSJNEf13C12 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 ATGAAAAGAACCGGAAGTGTATTTTCCTTGTAAACTGTAAAGAAAAGGAATAATGGAGGT 39
                                                                                                                                                                                                                        ATTGCATGTAAACAAGGTCATGATGTCTCTAAGCTGACACCTACTGATATTGCAATT
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                                                                                         CTTGCACAGCAAAGGGGTGATGCTTATGCAAATGCAGATGTAAGGGTTTCTCTCTGGAAGAG
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Bacterial

Bacterial
Herbicida
Bacterial
Arabidops
Bacterial
Bacterial
M. Catarr
Bacterial
DNA clone
Bacterial
Shikimate
Bacterial

Acinetoba Klebsiell Bacterial

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

Searched:

Database

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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A843182
A41142
A4114512
A410281
A4013793
A6827980
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ABB92451
ADS42564
AAG23897
ADS30077
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 Arabidopsis thaliana
25-FBB-1999;
05-MAR-1999;
09-MAR-1999;
25-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
06-APR-1999;
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23-APR-1999;
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum DB seq length: 2000000000
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9US - 0145918P 9US - 0144919P 9US - 014638EP 9US - 014638BP 9US - 014708P 9US - 014702P 9US - 0147102P 9US - 0147102P 9US - 0147102P 9US - 0147103P 9US - 0147103P	905 - 0149171P 905 - 0148319P 905 - 0148319P 905 - 0148368P 905 - 0149378P 905 - 0149723P 905 - 0149723P 905 - 0149723P 905 - 0149723P 905 - 0149930P 905 - 0149930P 905 - 0150884P 905 - 0150884P 905 - 0151066P 905 - 0151066P 905 - 0151069P	99135-0153738P. 99135-0154018P. 99135-0154013P. 99135-0155413P. 99135-0155438P. 99135-0155653P. 99135-0155653P. 99135-0155653P. 99135-0156438P. 99135-0156438P. 99135-0158232P. 99135-0158232P. 99135-0158232P. 99135-0158233P. 99135-0158233P. 99135-0158233P. 99135-0159233P. 99135-0159233P. 99135-0159233P. 99135-0159233P. 99135-0159233P. 99135-0159233P. 99135-0160767P. 99135-0160767P. 99135-0160767P. 99135-0160767P.	9US-0160969F 9US-0161404P 9US-0161405P
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9905-0134256P

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21-Jun-1999;
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22-Jun-1999;
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30-JUN-1999;
01-JUL-1999;
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24-JUN-1999
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                                                                                                                                                                                                                              79 LLKRKSEEVLFYLNGRCIYLVGMMGSGKSTVGKIMSEVLGYSFFDSDKLVEQAVGMPSVA
                                                                                                                                                                                                                                               OIFKVHSEAPFRDNESSVLRDLSSMRRLVVATGGGAVIRPINWRYMKRGLSVWLDVPLDA
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                                                                                                                                                        Length 303;
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                                                                                                                                                          DB 3;
                                                                                                                                                          43.3%; Score 660; DB 3; 63.1%; Pred. No. 2.7e-60
                                                                                                                                                                          Best Local Similarity 63.1%; Pred. No. 2.7e-
Matches 128; Conservative 35; Mismatches
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KNVSDLTPTEIAIEAFEQVLSFL 290
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99US-0123180P.
99US-0125788P.
99US-0126264P.
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99US-0126785P.
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99US-0128234P.
99US-0130449P.
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05-MAR.1999;
23-MAR.1999;
25-MAR.1999;
25-MAR.1999;
06-APR.1999;
06-APR.1999;
16-APR.1999;
116-APR.1999;
23-APR.1999;
23-APR.1999;
30-APR.1999;
30-APR.1999;
30-APR.1999;
66-MAY.1999;
06-MAY.1999;
06-MAY.1999;
25-OCT-1999;
26-OCT-1999;
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RR 25.-UUL-1999; 99US-0145214P.

RR 27.-UUL-1999; 99US-0145224P.

RR 27.-UUL-1999; 99US-0145224P.

RR 22.-UUL-1999; 99US-0145214P.

RR 22.-UUL-1999; 99US-0145214P.

RR 22.-UUL-1999; 99US-014531P.

RR 02.-MG-1999; 99US-014531P.

RR 02.-MG-1999; 99US-014531P.

RR 02.-MG-1999; 99US-0147302P.

RR 03.-MG-1999; 99US-0147302P.

RR 03.-MG-1999; 99US-0147302P.

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RR 13.-MG-1999; 99US-01431P.

RR 13.-MG-1999; 99US-01431P.

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RR 13.-MG-1999; 99US-014931P.

RR 25.-MG-1999; 99US-014931P.

RR 26.-MG-1999; 99US-014931P.

RR 27.-MG-1999; 9
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0
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990S-0123548P
990S-012568P
990S-0126785P
990S-0127462P
990S-0128714P
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990S-0130710P
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                                                                                                                                       Best Local Similarity 62.6%
Matches 127; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana.
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
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05-MAR-1999;
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990S-0142920P.
990S-0142977P.
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05-MAY-1999;
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13-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           96
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                                                                                                                                                                                                                                                                                                      42.6%; Score 650; DB 3; 62.7%; Pred. No. 2.3e-59;
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Best Local Similarity 62.7%; Pred. No. 2.3e
Matches 126; Conservative 35; Mismatches
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VSDLTPTEIAIEAFEQVLSFL 237
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99US-0159294P

99US-0159294P

99US-0159330P

99US-0159331P

99US-0159637P

99US-0159637P

99US-0159638P

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13-0CT-1999;
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29-SEP-1999;
04-OCT-1999;
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RRIAKVGTASRPLLDQPSGDPYAMAFSKLSMLAQQRGDAYANADVRVSLEEIACKQGHDD 260
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62.7%; Pred. No. 2.3e-59;
ive 35; Mismatches 40; Indels
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99US-0157753P.
99US-015865P.
99US-015823P.
99US-015823P.
99US-0159231P.
99US-0159231P.
99US-0159331P.
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99US-0159638P.
99US-016961AP.
99US-0160741P.
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Matches 126; Conservative
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990S-0134941P.
990S-0135124P.
99US-0135353P.
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99US-0137222P.
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99US-0139817P.
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99US-0140353P.
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 05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
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16-APR-1999;
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11-WAY-1999;
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04-MAY-1999
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   139 QIFKVHSEAFFRDNESSVLRDLSSMRRLVVATGGGAVIRPINWRYMKRGLSVWLDVPLDA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LARRIAKVGTASRPLLDQPSGDPYAMAFSKLSMLAQQRGDAYANADVRVSLEEIACKQGH 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoching them are useful for identifying modulators. The identified modulators are useful as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein identification, signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                           Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 LLKRKSEEVLFYLNGRCIYLVGMMGSGKSTVGKIMSEVLGYSFFDSDKLVEQAVGMPSVA
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                                                                                                                                                                                                                                        Claim 5; SEQ ID NO 1044; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          42.6%; Score 649.5; DB E 62.1%; Pred. No. 3.3e-59;
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KNVSDLTPTEIAIE-VSQVLSQLLHH 292
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28-AUG-2001; 2001WO-EP009892
                                28-AUG-2001; 2001WO-EP009892
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                                                                                              Weidler M;
                                                                                                                              WPI; 2002-269010/31.
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Best Local Similarity
                                                            (FARB ) BAYER AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 292 AA;
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28-SEP-1999;
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04-OCT-1999;
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156 VLRDLSSMRRLVVATGGGAVIRPINWRYMKRGLSVWLDVPLDALARRIAKVGTASRPLLD 215
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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99US-0162142P
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es 116; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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99US-0155486P.
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QVLSFL 186
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OPSGDPYAMAFSKLSMLAQQRGDAYANADVRVSLEEIACKQGHDDVSKLTPTDIAIESLH 275
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Gaps

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23-JUN-1999;
23-JUN-1999;
24-JUN-1999;
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05-AUG-1999;
06-AUG-1999;
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17-AUG-1999;
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 12280.
                              AAG12964 standard; protein; 199 AA
                                                                                                                                                                                               99US-0121825P

99US-0123180P

99US-0125788P

99US-012564P

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                                               AAG12964;
               RESULT 13
                        AAG12964
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121 DESGDAYSVAFKRLSAIWDERGEAYTNANARVSLENIAAKRGYKNVSDLTPTEICIEAFE 180
                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                            Arabidopsis thaliana protein fragment SEQ ID NO: 63308.
                                                                                              AAG49995 standard; protein; 194 AA
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Matches 115; Conserv
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31-AUG-1999;
01-SEP-1999;
10-SEP-1999;
113-SEP-1999;
15-SEP-1999;
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32; Mismatches 37
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ilarity 61.9%;
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Sequence 2087, Application US/09540236
Batent No. 6673910
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GENERAL INFORMATION:
TITLE OF INVENITON: NOCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATA-
TITLE OF INVENITON: POR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709,2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT APPLICATION NUMBER: US/09/540,236
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US-09-328-352-6149

Sequence 6149, Application US/09328352

Pacent No. 6562958

APPLICANT: GATUATION:
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPRENCE: GTO9-03PA

FILE REPRENCE: GTO9-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04
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Sequence 4, Appli
Sequence 8227, Ap
Sequence 6889, Ap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75; Indels 35;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258 HDDVSKLT----PTDIAIESLHKIESFVIEHTADSSASDAQAE 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --DIILTGRAYPKQMIGEILEVLENYALDHAPNKLKTDQHAK 228
US-09-568-486-7
US-09-568-472-7
US-09-568-472-7
US-09-828-062-9
US-09-568-402-4
US-09-568-486-4
US-09-568-486-4
US-09-568-486-4
US-09-568-486-4
US-09-568-486-4
US-09-568-486-4
US-09-358-472-4
US-09-358-472-4
US-09-358-472-4
US-09-349-016-7740
US-09-349-016-7740
US-09-252-991A-23627
US-09-252-991A-23627
US-08-500-857A-4
US-08-500-857A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.0%; Score 243.5; DB 4
30.9%; Pred. No. 1.3e-17;
tive 44; Mismatches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
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US-09-540-236-2087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 69; Conserv
     RESULT 1
US-09-540-236-2087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 231
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7;

Length 191;

70; DB 4;

212

81

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Squence 21964, Application US/09252991A
Facett No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US 60/074,788
FRIOR APPLICATION NUMBER: US 60/074,788
FRIOR APPLICATION NUMBER: US 60/094,190
FRIOR FILING DATE: 1998-02-18
FRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 FDSDKLVEQAVGMPSVAQIFKVHSEAFFRDNESSVLRDLSSMRRLVVATGGGAVIRPINW 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 RYMKR-GLSVWLDVPLDALARRIAKVGTASRPLLDQPSGDPYAMAFSKLSMLAQQRGDAY 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 QVLRAGGRVVYLHASVEHQIARTAR--DRNRPLLQKPNPGQI-----LRDLMALRDPLY 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLD--OPSGDPYAMAFSKLSMLAQQRGDAYANADVRVSLEEIACKQGH-DDVSKLTPTDI 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 LLQGVEPVRD------VLETLAEERNPLY------EEIADITIHTDDQSAKIVANQ 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66 GHEN----SHNSVDEALLLKRKSEEVLFYLNGRCIYLVGMMGSGKSTVGKIMSEVLGYSF
                                                                                                                                                                                                                                                                                                       23 RNIFLVGPMGAGKSTIGRQLAQQLSMEFYDSDQBIERRTG-ADVGWVFDVGGEGGFRQRB
                                                                                                                                                                                                                                                                                                                                                                         154 SSVLRDLSSMRRLVVATGGGAV-IRPINWRYMKRGLSVWLDVPLDALARRIAKVGTASRP
                                                                                                                                                                                                                                                                                                                                                                                                      82 EXIINELTEKQGIVLATGGGSVKSRETRNRLSARGVVVYLETNIEKQLARTQR--DKKRP
                                                                                                                                                                                                                                                                            94 RCIYLVGMMGSGKSTVGKIMSEVLGYSFFDSDKLVEQAVGMPSVAQIFKVHSBAFFRDNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13.5%; Score 205.5; DB 4;
illarity 32.8%; Pred. No. 1e-13;
Conservative 33; Mismarchor
                                                                                                                                                                                   13.9%; Score 212.5; DB 34.2%; Pred. No. 2e-14;
                                                                                                                                                                                                                              30, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas aeruginosa
PRIOR FILING DATE: 1999-04-09
                                                                                         TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                 64; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 AN-ADVRVSLEE 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 REIADVVVETDE 164
                   NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 6682
LENGTH: 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270 AIESLHK 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 IIELLEK 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 63; Conserv
                                                                                                                                                                                                         Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-252-991A-32964
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                                                                                                                         ; UKGANIAN: £10000
US-09-543-681A-6682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213
                                                                                                                                                                                        Query Match
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Patent No. 6605709
Patent No. 6605709
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABII
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT PAPLICATION NUMBER: US 60/128,706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10812, Application US/09489039A

Batent No. 6610813, Application US/09489039A

Patent No. 6610818

Batent No. 6610818

Batent No. 6610818

APPLICANT: Gary Breton et. al

ITILE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REPERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT PILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 RCIYLVGMMGSGKSTVGKIMSEVLGYSFFDSDKLVEQAVGMPSVAQIFKVHSEAFFRDNE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             154 SSVLRDLSSMRRLVVATGGGAV-IRPINWRYMKRGLSVWLDVPLDALARRIAKVGTASRP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LL--DQPSGDPYAMAFSKLSMLAQQRGDAYAN-ADVRVSLEEIACKQGHDDVSKLTPTDI 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32 IYLVGPMGAGKTTVGRHLAELLGREFLDSDHEIERKTG-ATIPWIFEKEGEVGFRTRETV 90
                                                                                                                                                                                                                                                         96 IYLVGMMGSGKSTVGKIMSEVLGYSFFDSDKLVEQAVGMPSVAQIFKVHSEAFFRDNESS
                                                                                                                                                                                                                                                                                                                                                   156 VLRDLSSMRRLVVATGGGAVIRPINWRYMK-RGLSVWLDVPLDALARRIAKVGTASRPLL
                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26; Gaps
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14.5%; Score 222; DB 4; Length 200;
1 Similarity 32.1%; Pred. No. 2.1e-15;
61; Conservative 36; Mismatches 67; Indels
                                                                                                                                                             Query Match
14.5%; Score 222; DB 4; Length 200;
Best Local Similarity 42.5%; Pred. No. 2.1e-15;
Matches 51; Conservative 27; Mismatches 38; Indels
                                                                      ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-6149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Klebsiella pneumoniae US-09-489-039A-10812
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6149
LENGTH: 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270 AIESLHKIES 279
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-489-039A-10812
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LENGTH: 200
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Indels

Length 184;

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98 LVGMMGSGKSTVGKIMSEVLGYSFFDSDKLVEQAVGMPSVAQIFKVHSEAFFRDNESSVL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 RDLSSMRRLVVATGGGAVIRPINWRYMKRGL-SVWLDVPLDALARRIAKVGTASRPLLDQ 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             217 PSGDPYAMAFSKLSMLAQQRGDAYANADVRVSLEEIACKQGHDDVSKLTPTDIAIESL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 NSKE-----ELVAIFQERQAWY-----EEVASRV--LDVTKLSPEEI-IEEL 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                            11.7%; Score 179; DB 4; Length 158; 34.8%; Pred. No. 5.5e-11; cive 27; Mismatches 63; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/ 085131
APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                    PRIOR APPLICATION NUMBER: US 09/107,433
PRIOR FLING DATE: 1998-06-30
PRIOR FLING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: US 60/085,131
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR APPLICATION NUMBER: US 60/051,553
PRIOR PLING DATE: 1997-07-02
SEQ ID NO 3547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: GTC-011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3398, Application US/09107433
Patent No. 6800744
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                         ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 159 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 3398:
2000-05-26
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STATE: Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 62; Conserv
  CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-09-107-433-3398
                                                                                                                                                                                                                                                                                                US-09-583-110-3547
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Patent No. 6699703
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
TITLE OF INVENTION: Pneumoniae for Diagnostics and Therapeutics
FILE REFERENCE: PATHO0-07A
CURRENT APPLICATION NUMBER: US/09/583,110
                                                                                            APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 IYLVGMMGSGKSTVGKIMSEVLGYSFFDSDKLVEQAVGMPSVAQIFKVHSEAFFRDNESS 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156 VLRDLSSMRRLVVATGGGAVIRPINWRYMK-RGLSVWLDVPLDALARRIAKVGTASRPL 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.2%; Score 185.5; DB 4; Length 178; 37.0%; Pred. No. 1.3e-11; tive 29; Mismatches 43; Indels 3
                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
FILING DATE: 30-Jun-1998
APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...178
SEQUENCE DESCRIPTION: SEQ ID NO: 5800:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                          ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                    Sequence 5800, Application US/09107532A Patent No. 6581275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                          STREET: 100 Beaver Street
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TELEFAX: (781)893-8277
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SEQUENCE CHARACTERISTICS:
LENGTH: 178 amino acida
TYPE: amino acid
                                                                                                                                                                       NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                              STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: ASCII
CURRENT APPLICATION DATA:
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
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Matches 44; Conservative
                                                                                                                                                                                                                                                                         CITY: Waltham
                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
US-09-107-532A-5800
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Best Local &
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Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT PILIGNG DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
RIOR APPLICATION NUMBER: 05 6012
SOFTWARE: PALENT: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PALENT: Nersion 3.1
LENGTH: 170
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                                                                                                                                                                                                                                                                                                                                                  158 RDLSSMRRLVVATGGGAVIRPINWRYMKRGL-SVWLDVPLDALARRIAKVGTASRPLLDQ 216
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                                                                                                                                                                                                                                                                                                                                                                                      61 ADLLOTDQ-VVSTGGGVVISQRNRDLLKTNTDNIYLKADFETLYQRIAADKDNQRPLFLN 119
                                                                                                                                                                                                                                                                                                6 IVLIGFMGAGKTTIGQSLANKLKMPHLDLDTALIEKIGR-SIPDYFEKYGBAAFREQETQ 64
                                                                                                                                                                                                                                                                                                                                                                                                                              217 PSGDPYAMAFSKLSMLAQQRGDAYANADVRVSLEEIACKQGHDDVSKLTPTDIAIESL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                               120 NSKE-----ELVAIFQERQAMY-----EEVASRV--LDVTKLSPEEI-IEEL 158
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                                                                                                                                                                                           / Match 11.7%; Score 179; DB 4; Length 159; Local Similarity 34.8%; Pred. No. 5.6e-11; Nes 62; Conservative 27; Mismatches 63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 11.0%; Score 167.5; DB 4;
1 Similarity 28.3%; Pred. No. 1e-09;
52; Conservative 38; Mismatches 73;
                                                          ORGANISM: Streptococcus pneumoniae
                                                                                              NAME/KEY: misc feature
LOCATION: (B) LŌCATION 1...159
SEQUENCE DESCRIPTION: SEQ ID NO: 3398:
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Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONGANISM: Enterococcus faecalis US-09-134-000C-4979
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 52; Conserv
                                                                                            NAME/KEY:
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                                                                                                                                                       US-09-107-433-3398
                                                                          FEATURE
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Matches
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APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABII
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR PAPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
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Patent No. 6610836
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PREMOVANIAE FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF ILING DATE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
LENGTH: 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 10.6%; Score 162; DB 4; Length 177; Similarity 35.5%; Pred. No. 4.2e-09; A3; Conservative 22; Mismatches 52; Indels
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                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53; Conservative
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Best Local Similarity
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US-09-489-039A-13538
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Sequence 3610, Application US/09134001C

Factoria 3610, Application US/09134001C

Factoria No. 6380370

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: UNMERS. US/09/134,001C
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1988-08-13

PRIOR APPLICATION NUMBER: US 60/064,964

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR APPLICATION NUMBER: US 60/055,779

PRIOR FILING DATE: 1997-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18195, Application US/09248796A

Sequence 18195, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION:
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT FILING DATE: 1999-02-13

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR APPLICATION NUMBER: US 60/096,409

RRIOR APPLICATION NUMBER: US 60/096,409

SRO ID NO 18195
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92 NGRCIYLVGMMGSGKSTVGKIMSEVLGYSFFDSDKLV---EQAVGMPSVAQIFKVHSEAF 148
                                                                                                                                                                                                         208 TASRPLLDQPSGDPYAMAFSKLSMLAQQRGDAYANADVRVSLEEIACKQGHDDVSKLTPT 267
                                                                                                                                                                                                                                                             126 LPER--LKE------AMKTKPLSEILTERID------RMKEIA-----DYI----- 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          156 VLRDLSSMRRL-VVATGGGAVIRPINWRYMKRGLS-VWLDVPLDALARRIAKVGTASRPL 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 YLK--SCINTFDIISTGGGIIEDTNSLKLLKNQKHVVWLDCDIEIIFKRVK--NDSHRPN 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 IILVGFMGTGKTTVGKYLSDLYNLSYVDLDNFIE-VNECKSIPNIFNDIGEKGFRSLETR 68
                                                                                                                                     7 NVMTIILCGLPTSGKSSLGKALAKFLNLPFYDLDDLIVSNYSSALYSSAEIYKAYGDQK
                                                                                                    149 FRDNESSVLRDLSSMRRLVVATGGGAVIRPINWRYMK-RGLSVWLDVPLDALARRIAKVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 AKSKNINQLDALYS--SRLSRYNEIAFWKVDSAQSVSEI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 LDQPSGDPYAMAFSKLSMLAQQRGDAYANADVRVSLEEI 252
                                                                                                                                                                                                                                                                                                              268 DIAIESLHKIESFVIEHTADSSASDAQAESQ 298
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US-09-134-001C-3610
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ORGANISM:
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                                                                 Sequence 1113, Application US/09198452A
Patent NO. 6559294
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT PILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      149 FRDNESSVLRDLSSMRRLVVATGGGAVIRPINWRYMK-RGLSVWLDVPLDALARRIAKVG 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          208 TASRPLLDQPSGDPYAMAFSKLSMLAQQRGDAYANADVRVSLEEIACKQGHDDVSKLTPT 267
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 NVMTIILCGLPTSGKSSLGKALAKFLNLPFYDLDDLIVSNYSSALYSSSAEIYKAYGDQK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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APPLICANT: Stephens, Richard
APPLICANT: Mitchell, Wayne
APPLICANT: Mitchell, Wayne
APPLICANT: Mitchell, Wayne
APPLICANT: Mitchell, Wayne
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
FILE REFERENCE: 018941-000411US
CURRENT APPLICATION NUMBER: US/09/438,185A
CURRENT APPLICATION NUMBER: US 60/108,279
PRIOR PELING DATE: 1998-11-12
PRIOR PELING DATE: 1999-11-12
PRIOR PELING DATE: 1999-04-08
NUMBER OF SEC ID NOS: 1074
SOFTWARE: FastSEQ for Windows Version 3.0
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9.4%; Score 143.5; DB 4
Best Local Similarity 26.5%; Pred. No. 4.2e-07,
Matches 56; Conservative 36; Mismatches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DIAIESLHKIESFVIEHTADSSASDAQAESQ 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 26.5%; Pred. No. 4.2e-
Matches 56; Conservative 36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1039, Application US/09438185A Patent No. 6822071
                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Chlamydia pneumoniae
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US-09-438-185A-1039
                        SULT 12
-09-198-452A-1113
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SOFTWARE: FASTS
SEQ ID NO 1039
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56 LRLRAKKSSGGHE---NSHNSVDEALLLKRKSEEVLFYLNGRCIYLVGMMGSGKSTVGKI 112 | : | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.2%; Score 125; DB 4; Length 276;
Best Local Similarity 26.4%; Pred. No. 7.2e-05;
Matches 33; Conservative 28; Mismatches 44; Indels 20; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: August 25, 2005, 11:17:53 Job time : 23 secs
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 GGGAV 175
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1526
1 MEAGGVGLALQARAAGFGSS......ADSSASDAQAESQIQRIQTL 305
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2: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
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10: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 10, Appl	Sequence 69542, A	Sequence 201135,	Sequence 201137,	Sequence 62604, A	Sequence 57834, A	Sequence 44984, A	Sequence 147803,	Sequence 28, Appl	Sequence 201136,	Sequence 187425,
OI OI	US-10-660-226-10	US-10-425-114-69542	US-10-425-115-201135	US-10-425-115-201137	US-10-425-114-62604	US-10-425-114-57834	US-10-767-701-44984	US-10-437-963-147803	US-10-660-226-28	US-10-425-115-201136	
DB	15	15	16	16	15	15	16	16	15	16	16
* Query Match Length DB	305	314	303	303	324	326	330	308	273	217	311
% Query Match	100.0	100.0	95.5	6.06	90.9	6.06	88.6	85.3	76.0	69.5	58.1
Score	1526	1526	1457	1387	1387	1387	1351.5	1301.5	1159	1061	886
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14	828	56.2	292	16	-10-425-115-2	
15	841	55.1	231	15	-10-660-	
16	733	48.0	199	16	US-10-739-930-10076	Sequence 10076, A
17	700	45.9	259	16	-10-437-	
18	625.5	Н	299	15	US-10-424-599-212900	
19	625.5	41.0	301	15	US-10-425-114-54946	
20	620	40.6	132	16	US-10-437-963-187427	
21	606.5	39.7	300	16	US-10-739-930-6067	
22	605	39.6	154	16	US-10-425-115-201132	
23	578.5	37.9	155	12	US-10-660-226-16	
24	547	35.8	120	12	US-10-425-114-52290	
25	535	35.1	170	15	US-10-424-599-280141	Sequence 280141,
56	535	35.1	170	12	US-10-425-114-54844	Sequence 54844, A
27	532.5	34.9	231	16	•	10480
28	504	33.0	152		US-10-767-701-42830	42830
29	423.5	27.8	220		US-10-424-599-212902	
30	409	26.8	163		US-10-424-599-168580	16858
31	405	26.5	92		US-10-424-599-205496	
32	374	24.5	103		US-09-864-408A-8602	
33	364.5	23.9	278		US-10-660-226-22	22, A
34	345	22.6	278	12	US-10-424-599-154207	
35	342	22.4	83	16	US-10-425-115-336215	Sequence 336215,
36	333	21.8	135	12	US-10-424-599-224958	
37	329.5	21.6	280	12	US-10-424-599-154203	
38	318.5	20.9	189	12	US-10-369-493-2620	2620,
39	316.5	20.7	188	15	US-10-369-493-19953	19953,
40	307	20.1	176	12	US-10-369-493-20994	20994
41	296	19.4	176	15	-10-424-599-2774	
42	294.5	19.3	134	12	-10-369-493	191
43	273	17.9	153	15	US-10-660-226-24	
44	270.5	17.7	138	16	US-10-767-701-39076	390
45	270.5	17.7	272	15	US-10-660-226-14	14,
					ALIGNMENTS	
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		0; Сарв	1 MEAGGVGLALQARAAGFGSSRHRGGLQAPTGSLRVADPAGPAVAVRARGSKPVAPLRLRA	MEAGGYGLALQARAAGFGSSRHRGGLQAPTGSLRVADPAGPAVAVRARGSKPVAPLRLRA
.611	305;	°,	SKPVA	SKPVA
(093)	Length 305;	18	RARG	RARG
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/лев УИВЕК , 199	15;		QAPTGSLRVADPAGPAVAVRARGS	DPAGE
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i26 .76	526;	tche	PTGS	PTGS
6 8ynth 660,2 4,501 RPPLJ DATE:	Score 1526; DB 15;	0; Mismatches	930102	361.02
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5/106 348A1 1 1 1 0 0 0 0 0 0 0 0 0 0 0 0 0	100.0%;	5	AGFGS	AGFGS
on U6 00644 beccc Carl Aliam Aliam ANDER UMBER: BER: 28 28 26 46 41 41 41 41 41 41 41 41 41 41 41 41 41		ಹ	OARA	OARA
Cation 1	1	Berv	GLAL	GLAL
Application US/1 Application US/1 C. US20040064848 MATION: Cahoon, Rebecca E Falco, S. Carl Fancdu, Layo O. Hitz, William D.	, ,	S	EAGG	EAGG
Sequence 10, Application US/10660226 Sequence 10, Application US/10660226 Publication No. US20040064848A1 GENERAL INFORMATION: PAPLICANT: Cahoon, Rebecca E. APPLICANT: Falco, S. Carl APPLICANT: Falco, S. Carl APPLICANT: Hitz, William D. APPLICANT: Hitz, William D. APPLICANT: Hitz, William D. APPLICANT: BB-1159-C CURENT PELING DATE: 2003-09-11 PRIOR APPLICATION NUMBER: US/10/660,226 CURRENT FILING DATE: 1999-07-16 PRIOR FILING DATE: 1999-07-16 PRIOR FILING DATE: 1999-07-16 PRIOR FILING DATE: BARLIER FILING DATE: J998 SOFTWARE: Microsoft Office 97 SEQ ID NO 10 ERGHT: 305 TYPE: PRT ORGANISM: Zea mays	Query Match	Matches 305, Conservative	Ξ-	Ζ-
-10-660-226-: Sequence 10, Sequence 10, Sequence 10, Sequence 10, APPLICANT: PRIOR PRIOR PLINW PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PLINW PRIOR	Query Match	hes		
US-10-660-226-10 Sequence 10, A Publication No GENERAL INFORM APPLICANT: F APPLICAN	Quer	Matc		•
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RIQTL 305
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ORGANISM: Zea mays
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ORGANISM: Zea mays
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Publication No. US20040034888A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jinddong
APPLICANT: Screen, Steven E
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Screen, Steven E
APPLICANT: Beneral Screen, Steven E
APPLICANT: APPLICANT: Candering Screen, Steven E
APPLICANT: APPLICANT: APPLICANT: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKSSGGHENSHNSYDEALLIKRKSEEVLFYINGRCIYIVGMMGSGKSTVGKIMSEVLGYS 120
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KKSSGGHENSHNSVDEALLLKRKSEEVLFYLNGRCIYLVGMMGSGKSTVGKIMSEVLGYS 120
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                  KKSSGGHENSHNSVDEALLLKRKSEEVLFYLNGRCIYLVGMMGSGKSTVGKIMSEVLGYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: UC-ZMFLB73062D01_FLI.pep
US-10-425-114-69542
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RESULT 4

US-10-425-115-201137, Application US/10425115
; Sequence 201137, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 201137
; LENGTH: 303
Sequence 201135, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Caso, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 201135
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Pred. No. 4e-134;
2; Mismatches 8; Indels 2.
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US-10-425-115-201135
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Best Local Similarity 96.1%;
Matches 293; Conservative ;
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Sequence 57834, Application US/10425114

Publication No. US2004034888A1

GENERAL INFORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Screen, Steven E

APPLICANT: Cao, Yongwei

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules Associated With

TITLE OF INVENTION: 18-21(53313)B

CURRENT PAPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 57934
                                                                                                                         ANADVRVSLEEIASKQCHGDVSKLMPTDIAIESLHKIESFVIEHAADNPASDSQAESQIQ 319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 MEAGGVGLALOTRAAPGSGORRGGLOSPIGRLRVAEPAGAAVAVRVRGSKPVVP--LRA
                                          200 WKYWKKGLSVWLDVPLDALARRIAKVGTASRPLLDQPSGDPYTWAFSKLSMLAEQRGDAY
                                                                                                 ANADVRVSLEEIACKQGHDDVSKLTPTDIAIESLHKIESFVIEHTADSSASDAQAESQIQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: UC-ZMFLB73191D05_FLI.pep
US-10-425-114-57834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 90.9%; Score 1387; DB 15; Best Local Similarity 91.1%; Pred. No. 3.3e-127; Matches 278; Conservative 9; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-767-701-44984
; Sequence 44984, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIQTL 305
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                                                                                                                                                                                     RIQTL 305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                             RESULT 6
US-10-425-114-57834
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Sequence 62604, Application US/10425114

Publication No. US20040034888A1

GENERAL INPORMATION:

APPLICANT: Liu, Jingdong

APPLICANT: Screen, Steven E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: Tabaska, Jack E

APPLICANT: TILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53313)B

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT FILING DATE: 2003-04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKSSGGHENLHNSVDEALLLKRKSEEVLFYLNGRCIYLVGMMGSGKSTVGKIMSEVLGYS 139
                                                                                                                                                                                                                                                                            KKSSGGHENLHNSVDEALLLKRKSEEVLFYLNGRCIYLVGMAGSGKSTVGKIMSEVLGYS 118
                                                                                                                                                                                                                                                                                                                                                                FPDSDKLVEQAVGMPSVAQIFKVHSEAFFRDNESSVLRDLSSMRRLVVATGGGAVIRPVN 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANADVRVSLEEIASKQGHGDVSKLMPTDIAIESLHKIESFVIEHAADNPASDSQAESQIQ 298
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                                                                                                                                                                                                                                                                                                                                       FFDSDKLVEQAVGMPSVAQIFKVHSEAFFRDNESSVLRDLSSMRRLVVATGGGAVIRPIN 180
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                                                                               Length 303;
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US-10-425-114-62604
                                                                             Score 1387; DB 16;
Pred. No. 3e-127;
9; Mismatches 16;
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               OTHER INFORMATION: Clone ID: MRT4577_115022C.1.pep
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                                                                             Query Match
Best Local Similarity 91.1%;
Matches 278; Conservative
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; FEALONG; OTHER INFORMATION US-10-425-115-201137
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US-10-425-114-62604
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LENGTH: 324
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                                                                                                                                                                                                                                               114
                                                                                                                                                                                                                                                                              60 P--LRAKKSSGGHETLHNSVDEALLLKRKSEEVLFYLNGRCIYLVGMMGSGKSTVGKIMS 117
                                                                                                                                                                                                                                                                                                                                                                                              VIRPINWRYMKRGLSVWLDVPLDALARRIAKVGTASRPLLDQPSGDPYAMAFSKLSMLAQ 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QRGDAYANADVRVSLEEIACKQGHDDVSKLTPTDIAIESLHKIESFVIEHTADSSASDAQ 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91 INGRCIYLVGMMGSGKSTVGKIMSEVLGYSFFDSDKLVEQAVGMPSVAQIFKVHSEAFFR 150
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                                                                                                                                                                                                                                               PLRLRAKKSSGGHENSHNSVDEALLLKRKSEEVLFYLNGRCIYLVGMMGSGKSTVGKIMS
                                                                                                                            1 MEAGGVGLALQARAAGF-GSSRHRGGL-----QAPTGSLRVADPAGPAVAVRARGSKPVA
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                                                                 Gaps
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      Length 308;
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   Query Match 85.3%; Score 1301.5; DB 16; Lengt
Best Local Similarity 86.2%; Pred. No. 7.4e-119;
Matches 268; Conservative 13; Mismatches 21; Indels
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GENERAL INPORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Fanco, Layo O.
APPLICANT: Rendina, Alan
TILE OF INVENTION: Chorismate Biosynthesis Enzymes
FILE REFERENCE: BB-1159-C
CURRENT APPLICATION NUMBER: US/10/660,226
CURRENT APPLICATION NUMBER: US/3-09-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0-116-0
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Best Local Similarity 85.5%; Pred. No. 6e-105;
Matches 235; Conservative 17; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Triticum aestivum
US-10-660-226-28
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ADSRAQRIQTL 308
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; Sequence 147803, Application US/10437963
; Bublication No. US20040123343A1
; GENERAL INPORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Cao, Vinua
; APPLICANT: Cao, Yongwei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Buchazuk, Brad
; APPLICANT: Li, Ping
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; TITLE OF EXPLICANT: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 147803
; LENGTH: 308
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yihua
TITLE OF INVENTION'S Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
FULE REFERENCE: 38-21(53535)B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     176 DNESSVLRDLSSMQRLVVATGGGAVIRPVNWKYMKKGLSVWLDVPLDALARRIAKVGTAS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPLLDQPSGDPYAMAFSKLSMLAQQRGDAYANADVRVSLEEIACKQGHDDVSKLTPTDIA 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LNGRCIYLVGMMGSGKSTVGKIMSEVLGYSFFDSDKLVEQAVGMPSVAQIFKVHSEAFFR 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

88.6%; Score 1351.5; DB 16; Length 330;
Best Local Similarity 83.3%; Pred. No. 1e-123;
Matches 279; Conservative 8; Mismatches 13; Indels 35;
                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C10471_1.pep
US-10-767-701-44984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: PAT_MRT4530_48297C.1.pep
US-10-437-963-147803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MEAGGVGLALQAR------
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ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Oryza sativa
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US-10-437-963-147803
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LENGTH: 330
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                                                                                                                                                                                                                                                                                                                                     60 VLPQGVQSFLIGLGEVVTFVVIWSKCDNLCVGNGVVQGHDSLHNSVDBALLLKRKSEEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -------MKYMKKGLSVWLDVPLDALARRIAQVGT
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                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                              90;
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                                                                                                                                                                                                                Length 311;
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                                                                                                                                                                                                                                                              49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Fanco, Layo O.
APPLICANT: Hitz, William D.
APPLICANT: Hitz, William D.
APPLICANT: Hitz, William D.
APPLICANT: Hendina, Alan
TITLE OF INVENTION: Chorismate Biosynthesis Enzymes
FILE REFERENCE: BB-1159-C
CURRENT APPLICATION UNBER: US/10/660,226
CURRENT FILING DATE: 2003-09-11
PRIOR FILING DATE: 1999-07-16
PRIOR FILING DATE: LOSSE CALLER APPLICATION NUMBER: 60/
PRIOR FILING DATE: EARLIER FILING DATE: J998
                                                                                                                                                                                                                                                                                                          1 MEAGGVGLALQARAA-GFGSS---RHRGGLQAPTG-SLRVADPAG
                                                                                                                                           j OTHER INFORMATION: Clone ID: PAT_MRT4530_84129C.1.pep
US-10-437-963-187425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IAIESLHKIESFVIEH-TADSSASDAQAESQIQRIQTL 305
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65.2%; Pred. No. 5.9e-77;
tive 33; Mismatches 49;
                                                                                                                                                                                                             Query Match 58.1%; Score 886; DB 16; Best Local Similarity 59.8%; Pred. No. 4.5e-78; Matches 202; Conservative 27; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 26, Application US/10660226; Publication No. US20040064848A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 26
LENGTH: 282
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 187425
LENGTH: 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Triticum aestivum
US-10-660-226-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 65.2%
Matches 180; Conservative
                                                                                               ORGANISM: Oryza sativa
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                                                                       TYPE: PRT
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TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
                                                                                                                                                                                                 Sequence 201136, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: Las Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Con, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT PILING DATE: 2003-04-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 FFDSDKLVEQAVGMPSVAQIFKVHSEAFFRDNESSVLRDLSSMRRLVVATGSGAVIRPIN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 KKSSGGHENSHNSVDEALLLKRKSEEVLFYLNGRCIYLVGMMGSGKSTVGKIMSEVLGYS 120
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  182 RPLLDQPSGDPYTWAFSKLSMLAEQRGDAYANADVRVSLEEIASKLGHDDVSKLTPIDIA 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MEAGGGGLALQARAAGFGSSRHRGGLQAPTGSLRVADPAGPAVAVRARGSKPVAPLRLRA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Clone ID: MRT4577_115021C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 WRYMKRGLSVWLDVPLDALARRIAXSGTASRPLLD 215
                                              271 IESLHKIESFVIEHTADSSASDAQAESQIQRIQTL 305
                                                                       181 WRYMKRGLSVWLDVPLDALARRIAKVGTASRPLLD 215
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OTHER INFORMATION: unsure at all Xaa locations
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Boukharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-425-115-201136
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US-10-437-963-187425
                                                                                                                                                                                          -10-425-115-201136
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LENGTH: 217
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 253534
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Publication No. US20040064848A1

GENERAL INFORMATION:

APPLICANT: Cahoon, Rebecca E.

APPLICANT: Falcon, Layo O.

APPLICANT: Remodu, Layo O.

PRIOR APPLICATION NUMBER: US/09/354,501

PRIOR APPLICATION NUMBER: EARLIER FILING DATE: J1998

NUMBER OF SEQ ID NOS: 28

SOFTWARE: MICTOROFE OFFICE 97

COLUMN: MONTH OFFICE OFFICE PRICE PRICE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: MRT4577_162804C.1.pep
US-10-425-115-253534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56.2%; Score 858; DB 16; 66.8%; Pred. No. 2.3e-75; iive 34; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 55.1%; Score 841; DB 15; Best Local Similarity 73.7%; Pred. No. 7.6e-74; Matches 165; Conservative 31; Mismatches 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   267 TDIAIESLHKIESFVIEHT 285
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Best Local Similarity 66.8*
Matches 173; Conservative
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ORGANISM: Zea mays
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                                                                                                             121 VEQSVGIPSVAEIFQVHSEAFFRDNESEVLRDLSSMHRLIVATGGGAVIRPINWSYMKKG 180
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                                                                                                                                                                                                                                                           VEQAVGMPSVAQIFKVHSEAFFRDNESSVLRDLSSMRRLVVATGGGAVIRPINWRYMKRG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                        188 LSVWLDVPLDALARRIAKVGTASRPLLDQPSGDPYAMAFSKLSMLAQQRGDAYANADVRV 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 AGPAL-----RP-AKLRVSCSAKSAGTGKVHYSTDEALILQQKAQDVLPYLDGRCVYL
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; Sequence 20, Application No. US20040064848A1
; Sequence 20, Application No. US2004006484BA1
; GENERAL INFORMATION:
    APPLICANT: Cahoon, Rebecca E.
    APPLICANT: Palco, S. Carl
    APPLICANT: Pamodu, Layo O.
    APPLICANT: Pamodu, Layo O.
    APPLICANT: Rendina D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 56.4%; Score 860; DB 15; Length 245; Best Local Similarity 70.4%; Pred. No. 1.1e-75; Matches 174; Conservative 32; Mismatches 33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               241 SLENIAFKQGHNDVNVLTPSAIAIEALLKMESFLTE 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLEEIACKQGHDDVSKLTPTDIAIESLHKIESFVIE 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ||: | |
235 SFLTEKT 241
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US-10-425-115-253534
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The Rice Full-Length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-Length cDNA Project Team:, Kikuchi,S., Satoh,K., Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J., Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T., Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Li,C., Ohtsuki,K., Li,C., Ohtsuki,K., Li,C., International Science Genome Sequencing & Analysis Group:, Otomo,Y., Murakami,K., Iida,Y., Sugano,S., Fujimura,T., Suzuki,Y., Tsunoda,Y., Murakami,K., Narikawa,R., Sugiyama,A., Mizuno,K., Yokomizo,S., Niikura,J., Ikeda,R., Ishibiki,J., Kawamata,M., Yoshimura,A., Miura,J., Kusumegi,T., Oka,M., Ryu,R., Ueda,M., Matsubara,K., Rikkin:, Kawai,J., Carninci,P., Adachi,J., Alazawa,K., Rikkin:, Kawai,J., Carninci,P., Adachi,J., Alazawa,K., Ishii,Y., Itoh,M., Hayatsu,N., Imotani,K., Ishii,Y., Itoh,M.,
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AR06577 Gloeobact
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AR017161 Prochloro
BT012132 Arabidops
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Oryza siva (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae;
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-USECORE=D1/USFO spool/US10660226/runat_25082005_110427_28529/app_query.fasta_1.455
-DS=GenEmb1 -QFWT=fastap -SUFFIX=rge -MINNATCH=0.1 -LOOFCL=0 -LOOFEXT=0
-UNITS=bite -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN-E -ALIGN=15 -MODE=LOCAL
-UNFRYT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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Copyright (c) 1993 - 2005 Compugen Ltd.
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NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
Konno,H., Miyazaki,A., Osato,N., Ota,Y.,
Sato,K., Shibata,K., Shinagawa,A., Shiraki,T.,
                                                                             over 28,000 cDNA clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602, Japan (E-mail:skikuchi@mas.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)
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/mol_type="mRNA"
/cultivar="Nipponare"
/db ref="taxon:39947"
/clone="J013074E04"
                                                                           Collection, mapping, and annotation of japonica rice Science 301 (5631), 376-379 (2003)
  Kagawa, I., Kondo, S., Konno, H.
Saito, R., Sasaki, D., Sato, K.,
Yoshino, M. and Hayashizaki, Y.
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Db 245 AAGATCTTGGCTGAAGTTTTGGCTTATCTTCTTCGACAGTGATAAATTGGTCGAACAA 304 31 AlaValGlyMetProSerValAlaGln ebbclygValHisSerGluAlabheArg 150 305 GCTGTTGGCATGCTCAAATTTCAAGGTTCATAGTGAAGCCTTCTTCAGA 364 Oy 151 AspAsnGluSerSerValLeuArgAspLeuSerSerMetArgArgAGCCTCTTCAGA 364 Oy 151 AspAsnGluSerValLeuArgAspLeuSerSerMetArgArgArgCTCTTCAGA 364 Oy 171 GlyGlyGlyAlaValIleArgPrOILeASATGCTCCTCAATGCGGCGATTAGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGT	211 ArgProLeuLeuAspGlnProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSer	271 IleGluSerLeuHisLysTleGluSerPheVallleGluHisThralaAspSerSerala :::	RESULT 3 AK109730 LOCUS LOCUS LOCUS AK109730 LOCUS AK109730 AK100730 AK10730 AK100730 AK100730 AK100730 AK100730 AK100730 AK100730	Kurosaki, T., Kodam, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Murra, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Murra, J., Kusumegi, T., Oka, M., Ryu, W., Ueda, M., Matsubara, K., RIKEN: Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatus, N., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Myazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M. and Hayashizaki, Y. TITLE Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice JOURNAL Science 301 (5631), 376-379 (2003)
Qy 243 aAspValArgValSerLeuGluGluIleAlaCysIvyGlnGlyHisAspAspValSerLy 263 Db 1007 TGATGTGAGGGTTTCTCTTGAAGAGATTGCATCTAAACAGGGTCATGATGATGATCGAA 1066 Qy 263 sLeuThProThrAspIleAlaIleGluSerLeuHisLysIleGluSerPheValIleGl 283 Db 1067 GCTAACACCAACTGAATTGAGTGTTCATAAGATCGAAATCGAAATCGAAATCGAAATCGAAATCGAAATCGAAATCGAAATCGAAATTGATTTCATAATAATTGATTTCATAAATGAATCGAAATCGAAATCGAAATCGAAATCGAAATCGAAATCGAAATCGAAATCGAAATCGAAATCGAAATCGAAATCGAAATCGAAATCGGTTGATGATGATGATGATGATGATGATGATGATGATGAT	RESULT 2 BT009529 LOCUS LOCUS LOCUS BT009529 LOCUS DEFINITION Triticum aestivum clone wrl.pk0122.a1:fis, full insert mRNA SEQUENCE. ACCESSION BT009529.1 GI:32129080 VERSION BT009529.1 GI:32129080 VERSION FILE CDNA. Triticum aestivum (bread wheat) ORGANISM Triticum aestivum (bread wheat) SOURCE ORGANISM Triticum Aestivum (bread wheat) SCHENCE ORGANISM Triticum Aestivum CRANDICH ORGANISM Triticum Aestivum SCHENCE ORGANISM Triticum Aestivum CRANDICH ORGANISM TRITICUM AESTIVUM AE	Pooldeas, Triticeas, Triticum. S Tingey,S.V., Wolters,P., Powell,W., Dolan,M., Miao,GH Caraher,N.R., Hanafey,M.K. and Hainey,C.F. Direct Submission L Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de USA	PERTURES Location/Qualifiers	71 HisbanServalAspGluAlaLeuLeuLeuLysArgLysSerGluGluValLeuPheTyr 71 HisbanServalAspGluAlaLeuLeuLeuLeuLysArgLysSerGluGluValLeuPheTyr 125 CataAcrcGGTGAGGAGGAGGAAAATCAGAAGAGGTTCTTTTCCAG 91 LeuAsnGlyArgCysIleTyrLeuValGlyMetMetGlySerGlyLysSerThrValGly 185 TTGAACGGTGGTTCTTAGTAGAATGATGGATGGGTTCTTTTCAG 111 LysIleMetSerGluValLeuGlyTyrSerPhePheAspSerAspLysLeuValGluGlu 111 LysIleMetSerGluValLeuGlyTyrSerPhePheAspSerAspLysLeuValGluGlu 111 LysIleMetSerGluValLeuGlyTyrSerPhePheAspSerAspLysLeuValGluGlu

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US-10-660-226-10 (1-305) x AK109730 (1-1918)
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3. Hangaki, T., Harah, Hashizume, W., Hiraoka, T., Hayashida, K., Hayashida, Y., Hayashida, Y., Hayashida, Y., Hayashida, Y., Hashida, J., Hamura, K., Harancto, K., Harancto, K., Harancto, K., Harancto, K., Harancto, Y., Kadawa, I., Kanagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kanagawa, I., Kodama, T., Kojima, K., Kojima, Y., Kodama, T., Kojima, K., Kojima, Y., Kodama, T., Komo, H., Kodama, M., Kodama, T., Murakami, K., Marsuwa, T., Midra, J., Miyaza, M., Masuda, H., Matsubara, K., Matsuyama, T., Midra, J., Miyaza, M., Masuda, H., Marshami, K., Muraka, M., Midra, J., Miyaza, M., Mixuno, K., Mixuno, M., Ostaki, K., Mixuno, M., Ostaki, K., Ostaki, K., Ostaki, K., Satoh, K., Satoh, K., Shibata, K., Satoh, K., Shibata, K., Shibata, K., Satoh, K., Shibata, K., Satoh, K., Shibata, K., Satoh, K., Satoh, K., Shibata, K., Satoh, K., Satoh, K., Shiraki, T., Tsunoda, Y., Tsunoda, Y., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomada, H., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.

Direct Submission

Direct Submission

Direct Submission

Direct Submission

Submitted (27-AuG-2002) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tuukuba, Ibaraki Jabraki Glene Expression; 2-1-2 Kannondai, Tuukuba, Ibaraki Jabraki Chone Is one of the 28K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Falls Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fulls Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fulls Genome Sequencing & Islain, T., Kusumega,M., Kobayashi,M., Kodayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,M., Miqara,J., Mizuno,K., Narikawa,R., Nikukra,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Masubara,K. and Mirzkami,K. Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninoi,P., Fukuda,S., Hanamoto,K., Hara,A., Hashizume,W., Hayashida,K., Hayatu,N., Hiramoto,K., Hiraoka,T., Kanagawa,T., Imamura,K., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kanagawa,T., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyam,T., Miyazaki,A., Murata,M., Nakai,K., Nomura,K., Nimasaki,R., Ohno,M., Osato,N., Ota,Y., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sagabe,Y., Tagami,M., Tagami,Takeda,Y., Tagawa,A., Takahashi,F., Yasunishi,A. and Hayashizaki,Y. Tomaru,A., Toya,T., Waki,K., Yasunishi,A. and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           URL: http://cdna01.dna.affrc.go.jp/cDNA/
NIAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satoh,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T. and
Yamamoto,M.
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/mol type="mRNA"
/cultivar="Nipponbare"
/cultivar="1 axon: 39947"
/clone="002-146-B12"
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1163 AAGTTGGTTGAACAAGCAGTTGGAATGCCTTCTGTTGCCCAAATATTCAAGGAGCACAGT 1222
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Triticum aestivum clone wrl.pk0099.bl2:fis, full insert mRNA
                                                                                                                                                                                   1043 GAAGTICTATICTACTIGAACGGACGGIGIATITATITAGTIGGAATGAIGGCTCAGGG 1102
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|1643 ||||:::
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Eukaryowan accounts.

Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Oldeae; Triticam.

(Dases 1 to 1323)

Tingey,S.V., Wolters,P., Powell,W., Dolan,M., Miao,G.-H.,

Caraher,N.R., Hanafey,M.K. and Hainey,C.F.

Direct Submission

Submitted (20-UUN-2003) Crop Genetics, E. I. DuPont de Nemours and
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                                                                                                                                                                                                                                                                                                                                                                          145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 LeuValValAlaThrGlyGlyGlyAlaVallleArgProlleAsnTrpArgTyrMetLys 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    186 ArgGlyLeuSerValTrpLeuAspValProLeuAspAlaLeuAlaArgArgIleAlaLys
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GlyHisGluAsnSerHisAsnSerValAspGluAlaLeuLeuLeuLysArgLysSerGlu
                                                                                                                                                                                                                                                LysSerThrValGlyLys1leMetSerGluValLeuGlyTyrSerPhePheAspSerAsp
                                                                                                                                                                                                                                                                                                                                                                          LysLeuValGluGlnAlaValGlyMetProSerValAlaGlnIlePheLysValHisSer
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                                                                                                                             GluValLeuPheTyrLeuAsnGlyArgCysIleTyrLeuValGlyMetMetGlySerGly
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Agrobiological Resources, Rice Genome Research Program; Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan (E-mail: tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/, Tel:81-298-38-7441, Fax:81-298-38-7469)

The nucleotide sequence of this BAC clone was generated by combining Monsanto and RGP-Japan sequencing data.

NOTE: It currently consists of I contiges Gaps between the contiges are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
                                                                               Oryza sativa (japonica cultivar-group) chromosome 2 clone
OJ1308 A10, *** SEQUENCING IN PROGRESS ***.
                                                                                                                                                                                                        Oryza satīva (japonica cultivar-group)
Oryza satīva (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 SerArgHisArgGlyGlyLeu------GlnAlaProThrGlySerLeuArg
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Direct Submission
Submitted (22-AUG-2001) Takuji Sasaki, National Institute of
                                                                                                                                                                                                                                                                                                                                                BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Oryza sativa (japonica cultivar-group)"
| mol type="genomic DNA"
| cultivar="Nipponbare"
| db_xref="taxon:39947"
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263
14
25
512
                     829
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Oryza sativa nipponbare(GA3) genomic DNA,
Clone:OUT308 Alo
Published Only in Database (2001)
2 (bases 1 to 111777)
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Mismatches:
Indels:
793 TGAGGCATTGCTAAAGATGGAGAGCTTTCTTACTGAG
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/clone="0J1308_A10"
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34.24%
32.51%
54.82%
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Best Local Similarity:
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AP004089/c
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VERSION
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   Box 6104, Newark, DE 19714-6104,
                                                                                                                                                                                                                                                                                                                                                                                      14 AlaAlaGlyPheGlySerSerArgHisArgGlyGlyLeuGlnAlaProThrGlySerLeu
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Conservative:
Mismatches:
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Company, 1 Innovation Way, P.O.
USA
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881.50
78.75$
67.03$
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Best Local Similarity:
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Pred. No.:
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join(<747. .1033,1549. .1595,1683. .1737,1842. .1914,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (join(10085. .10456,10633. .10695,10796. .1091;
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13791. .13835,14487. .14573,14661. .14744,14864. .15043,
15122. .15262,15433. .15541,15971. .16026,16477. .16484,
16581. .16719,17270. .17377,17698. .17724,17885. .17977,
18397. .18476,18611. .18700,18846. .18936,19063. .19354,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        // gene="P0431B06.3"
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// notes="P0431B06.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="start and end point are not identified" complement(join(6499. .6558,6932. .7039,7135. .7255,7669. .7930)) / gene="P0431B06.3"
                                                                                                                                                                                                                                                   /note="supported by full-length cDNA(s): AK066687"
747. .3402
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                                                                                                                                                                                                                                                                                                                                                                                                                         probably inactive due to 3'UTR too long in CDS" complement(4342. .4808)
/gene="P0431B06.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (4442. .4759)
/gene="P0431B06.2"
/note="contains full-length cDNA(s): AK058B32"
                                                                                                                                                                                                                                                                                                                                                      /note="contains full-length cDNA(s): AK066687 non-coding transcript
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YGENESKKGVDVGSE"

Join (9079. 9119,9183. 9349,9987. 10000)

/gene="P0431B06.4"

join (9079. 9119,9183. 9349,9987. 10000)

/gene="P0431B06.4"
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contains full-length cDNA(s): AK119455"
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/product="unknown_protein"
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/gene="P0431B06.2"
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/gene="P0431B06.5"
                                                                                                                                                                                                 3141. .>3402)
/gene="P0431B06.1"
                                                                                                  /gene="P0431B06.1"
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                                 clone="P0431B06"
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Sasaki, T. Matsumoto, T. and Yamamoto, K. Direct Submission

Al Submitted (30-FBS-2002) Takuji Sasaki, National Institute of Submitted (30-FBS-2002) Takuji Sasaki, National Institute of Agrobiological Sciences, Rice Genome Research Program; Kannondai 2-1-2, Taukuba, Ibaraki 105-8602, Japan

(E-mail:tesasaki@nisa.affrc.go.jp, WELintp://rgp.dna.affrc.go.jp/, Tel.381-298-38-7468)

On Apr 14, 2004 this sequence version replaced gi:33468820.

Genes were predicted from the integrated results of the following: GENSCAN (http://ccR-081.mit.edu/GBNSCAN.html), FGENESH

(http://www.igr.org/tdb/glimmerm/glmr_form.html), FGENESH

(http://www.igr.org/tdb/glimmerm/glmr_form.html), RiceHMM

(http://pobal.biology.gatech.edu/GeneMark), GlimmerM

(http://pobal.biology.gatech.edu/GeneMark), glimcePredictor (http://pobal.biology.gatech.edu/GeneMark), glimcePredictor (http://ploinformatics.isatate.edu/GeneMark), glimcePredictor (http://globin.cse.psu.edu/html/docs/sim4.html), gap2

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63571 CGAGAACTTTGTCATTGAACATACCGTTGACAATCCGGTTGGTGACTCCCAGGCTGACTC 63512
                                                                                                                                                                                                                                             Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 2, PAC clone: P0431B06.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, PAC
clone:P0431B06
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Oryza sativa (japonica cultivar-group)
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
                                                            297 rGlnIleGlnArgileGlnThrLeu 305
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                                                                                                                                               20 SerArgHisArgGlyGlyLeu------GlnAlaProThrGlySerLeuArg
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IRKAVEARPOKLLTELVFSEDLMBALEBAKAIGDELGDIYDYVAPCFPPRYEIFQLMV
YYTERPIQMALLISDRANDIPNINILKYTGMVVKYQENLLGGAVDESLAQVCSESGA
LDPLMNMYVERMQATTKKWYSNILEADKTQPPKSTEDGKLYTPAAUDLFRILTEQVQI
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KDWMEGMYTELYJATFADYFGDYKQYIERSRFRFYBACLEGTIYVYYDHLLYQKGHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LMTKRGTKVKVLEYGTVVEVVFHDLSSENHPMHLHGFAFYVVGRGNGTFDESRDPATY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nlvdppfqntvsvprsgwaairfradnpgvwfmhchfdrhvvwgmdtvfivkdgktpq
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263
14
25
512
13
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AQMLPRPPNMPOC"
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836.50
34.24%
32.51%
54.82%
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
Pred. No.:
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1897

119 TyrSerPhePheAspSer----

g 8

US-10-660-226-10 (1-305) x AP004774 (1-154796)

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                                                                                                                                                                                                                                                                   /translation="Magrggpgbaarwollaagdvaggaagaahggpgbaawrcagala
agggagdaaagbvaglrggggrgbggggrrb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                this category is not included in IRGSP standard" 28959. 29387 (Jene="0SJNBa0078N11.10" / join (C28559. 29126,29274. >29387) / Jene="OSJNBa0078N11.10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       predicted by GENSCAN
this category is not included in IRGSP standard"
join(28381. .28444,28479. .28567)
join(28381. .28444,28479. .28567)
join(28381. .28444,28479. .28567)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="5' terminal repeat"
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32826. 34707
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'codon start=1
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The orientation of the sequence is from M13rev to -21M13 of the BAC clone. This sequence of OSJNBB0078M11 clone has an overlap with OSJNBB0024K03 (DDBJ: AP006733) clone at 5' end and with P0431B06 (DDBJ: AP004774) at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.and.affrc.go.jp/GenomeSeq.html.
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predicted by GENSCAN
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15790. .16489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
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		146676 CA-GGAATGATGAGTTCTGGAAAAGTACTGTGGGAAAGATCATGTCTGAAGTTTTGGGT 146734 119 TyrSerPhePheAapSer124		125BPDLyBLeuValGlu 129 146794 GCTCATGGTAATCTAAGCTTTTATATTTCTGGAATTGTTTGCAGTGATAAATTGGTCGAA 146853	130 GlnalaValGlyMetProSerValAlaGlnIlePheLysValHisSerGluAlaPhePhe 149 	150 ArgaspasnGlu 153 146914 AGGGATAATGAGGTAATCTTTTTTTTTCTGAATCCATCTTCTGCTAACATGATCTACTATCT 146973	153 153 153 146974 TAGCATTTGTTACTGTAGGAAAATCTGAGACTGATTATTTTCTCTGTG 147033		GCTCTTTTTATGCGATTACAGAGTAGTGTCTTGAGGGATTTGTCCTCAATGAAGCGATTA	16/ Valvaladintriputyolyalavalilieargeroileannip 181 	181	TCTATTTTCCTGTTGGAATAGTTTATTTTGTGGCTTCTCTTATTTTGAATAACAATATT	182	193 pValProLeuAspAlaLeuAlaArgArgIleAlaLysValGlyThrAlaSerArgProLe 213	uleuAspGlnProSerGlyAspProTyrAlaMetAla	147334 TCTAGATCAACCATCTGGTGATCCATACACAATGGT-GACTACTTGGCCCATGAATTAT 147392	GCCATGCATGAATATGATATTATTCAGATGTATTTTTTAAATTTTTAATCAGTCAATA	225 225 147453 TACCTTCATTCATTCTACAAATGAAAAACAAAAACTTCCAAGTATGATCTTCCACATTCTCC 147512	resection items of a management of the constitution of the constit	147513 AACTGGTAGTGTAATTCTTTCATTTCAGTGCTAGTATGAGTTGCTCACTGGATTCTTCCT 147572	226PheSerLyBLeuSerMetLeualadlnGlnArgGlyAspAlaTyrAlaAs 242 	nAlaAspValArgValSerLeuGlu
- i	8 8 8 8	a &	qq	දුරු දුර	& 8 €	& A	9 Q	ò	옵 &	충 음	ò	qa (A 선	ò á	8 8	음 &	3 A	8 8	8 &	ପ୍	& g	È
opnaed/	Alignment Scores: Pred. No.: 836.50 Matches: 263 Score: 836.50 Matches: 263 Matches: 27.2.51 Length: 14 Best Local Similarity: 32.51 Mismatches: 25 Query Match: 84.82 Indels: 512 BB: Gaps: 13	-10-660-226-10 (1-305) x AP005848 (1-155168)	Qy 1 MetGlualaGlyValGlyLeuAlaLeuGlnalaArgAlaAlaGlyPheGlySer 19 Db 145666 ATGGAGGCGGGCGTGGGGCTGCAGTGCGCGGGGGTTCGGCGGCTCC 145722	Qy 20 SerArgHisArgGlyGlyLeu	A	55 ProteutrgleutrgalalystysSerSerGly	99	Db 145896 CGTTCTGTCAGATTGGTTGATTTGGCAAAAGTTTGTTTTTGTTTTTGACGAACTGGCG 145955 Qy 65	145956 GTCTGGCGCCATTTGGGCCCCTTTTTTGTGTGTGTCCGATTTTGTCGATCGGGATTGTTG	29	Db 146016 ATATTTGGAGGAACACATGGAACGGGTGCGTTGATTCGGTCAAAAAAAA	146076 GCAAGTAAGGAATTAGGTGGTAAGGCTGGCTTCGAATGGATCGAATACTGCAAAAGTTGT	Qy 65	39	Db 146196 TTGTTCGGATTAGATTGATCAAAATGGATAGGTTGATTGGGATTATTGGAAAGGTAG 146255 Qy 65	Db 146256 GAAGAAGATGAAGTTTCGCCTATGATTGGTCCTTCTAGATCAAGCCAATCCTGAAAATTCC 146315		Qy 66GlyHisGluAsnSerHisAsnSerValAspGluAlaLeuLeuLeuLys 81	146376 TCCTGTGCAGGTCATGAACATTGCATAACTCGGTTGATGAAGCCCTCTTGCTAAAGGTA	Oy 81 81 Db 146436 CTGCATAATCAAATCAAAGCGACACTGGAGTTTGCTTGTTTTCTTCCATCACTCTATGT 146495	82	Db 146496 TCTAACCATCTGTTTTTTCAGAGAAATCAGAAGAGTTCTCTTTTTTAAATGGA 146555 Qy 94 ArgCysIleTyr97

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BLASTN with the corresponding DDBJ accession no.

A gene with identity or significant homology to a protein is classified based on the protein name to indicate the homology level such as same name, 'putative-, and 'like protein'. A gene without EST homology (covering almost the entire length of partial sequence) is classified as an 'unknown' protein, A gene predicted by two or more gane prediction programs is classified as a 'hypothetical' protein according to IRGSP standard. A gene predicted by a single gene prediction program is also classified as a probable 'hypothetical' protein and is included as a miscellaneous feature of the sequence. Is from SP6 to 77 of the PAC clone. The orientation of the sequence is from SP6 to 77 of the PAC clone. This sequence of P0690H04 clone has an overlap with P0638H11 clone (DDBJ: AP005545) at 5' end and an overlap with P0425F05 (DDBJ: AP003569) at 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://rgp.dna.affrc.go.jp/GenomeSeq.html.
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BENYBDWYGADANGYRRGSWERHILAVYXISERKIAARWPLMKTLKWSDABARI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="msflldmfydvlasiglwgkeakilflgldnagkttlfymlsge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="supported by full-length cDNA(s): AK104692" 9586. 11016
/gene="P0690H04.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="supported by full-length cDNA(s): AK071845" complement(6801. .8015)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="supported by full-length cDNA(s): AK067095"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="mitochondrial transcription termination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="start and end point are not identified" join(2403. .2534,2937. .3068,5832. .6152)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="PO690H04.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oin(<2403. .2534,2937. .3068,5832. .>6152)
gene="P0690H04.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="small GTP-binding protein"
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/db_xref="GI:51535001"
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/gene="P0690H04.2"
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/gene="P0690H04.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:39947"
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/gene="P0690H04.3"
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/gene="P0690H04.3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="P0690H04"
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Listed (11-74PR-201) Takuji Sasaki, National Institute of
Direct Submission

Submitted (11-74PR-201) Takuji Sasaki, National Institute of
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2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail: tsasakiānias as fafrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel: 81-298-38-7441, Fax.81-298-38-7468)

On Feb 5, 2004 this sequence version replaced gi:13603473.
Genes were predicted from the integrated results of the following:
GENSCAN (http://CRR-081 mit-edu/GENSCAN.html), FGENESH

(http://www.softberry.com/), GeneMark.htm

(http://www.tigr.org/tdb/glimmerm/glmr_form.html), RiceHMM

(http://pgi.biology-gatech.edu/GeneMark.k), GlimmerM

(http://pgi.biology-gatech.edu/GeneMark.k), glimmerm

(http://www.tigr.org/tdb/glimmerm/glmr_form.html), sim4

(http://globin.cse.psu.edu/html/docs/sim4.html), gap2

(http://www.tigr.org/software/glimmerm/gl), BLASTN and BLASTN. The
genomic sequence was searched against NCBI NonRedundant Protein database

nceions were searched against NCBI NonRedundant Protein database

with BLASTP. ESTS represent the identified CDNA sequences using

BLASTN with the corresponding DDBJ accession no. and RGP clone
Full-length cDNAS represent the identified CDNA sequences using
            147633 TGCTGATGTGAGGGTTTCTCTTGAAGGTATAACTTCACAAGTTTTTCGCAAATCCGCGCT 147692
                                                                                                                                  147693 TTCCCATTTAGAGAATATGTGCTAGGTTATGTGCGACACATTACTTTTAAGTAATGCTTG 147752
                                                                                                                                                                                                                                                     147753 ATAACTCCATTTTTCCCTGCATAGAATAACATATGTTTTTGGAACTTGCAGAGATTGC 147812
                                                                                                                                                                                                                                                                                                                                                   147813 ATCTAAAACAGGGTCATGATGATGGAATGGAAGCTAACACCAACTGACATTGCTATTGAGGT 147872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       147932 AACGTACTGAAACAATTTCCCTAACAATTCTTGGCATTTTACAGTCGTTTCATAAGAT 147991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arvujsl3 137319 bp DNA linear PLN 25-AUG-2004 Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 6,
                                                                          .----- 250
                                                                                                                                                                                                                                                                                                                aCysLysGlnGlyHisAspAspValSerLysLeuThrProThrAspIleAlaIleGluSe 273
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                             ----GluIleAl
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Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, PAC
clone:P0690H04
Published Only in Database (2001)
2 (bases 1 to 137319)
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AP003513.2 GI:42415338
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VERSION
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TITLE
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JOURNAL
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SOURCE
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23576 ACAACATGACACTGTTATTTTCAGATAGTTTCTATTTTTTTGTAGTGATTTGAATGGAA 23517
                                                                                                                                         /translation="MPSALPPRHTQAPAPAAASASACLLRRRRGRLRVSLCYCRAST
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complement (18161. .19000)
                   /note="contains full-length cDNA(s): AK109268 similar to Arabidopsis thaliana chromosomes, At5g09995"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66 GlyHisGluAsnSerHisAsnSerValAspGluAlaLeuLeuLys-------24116 GGCCACGACGACGATGATAACTCAGTTGATGAAGCCCTCCTGTTAAAGGTAAATAACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23876 TGTATCATTTAATTGTTAACCTGTAACTGGAGACTAAATACCAAGTTAAATATAACTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23456 TTGTCTAACAGAGTAGTGTCTTGAGGGACTTGTCCTCAATGCGACGATTAGTTGTTGCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23996 TCATCTTTGGCTTTCGGCCATTGGTATAATGTTTTCTAATTGTAATTGCAGGGAAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24056 TTACAAAAATTCCTACTATTAGTTAAATCAAGAGTAAAATATGGCTAGAACTTTGTTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              yLysSerThrValGlyLysIleMetSerGluValLeuGlyTyrSerPhePheAspSerAs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23516 AGATTTGTGGAGTAACAATTTCTCAGACATGATAGACTAACAATTCCATGGTTCCCTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 hrGlyGlyGlyAlaValIleArgProIleAsnTrp------
                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
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  gene="P0690H04.6-1"
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                                                               /codon_start=1
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48.03%
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Speppayedylvatwgltgaqarkaskkishlrspsksdavlaflsblglpprkiaav
Atadprflcadvesnlarrvdelgglglsrrqjarlyplaltcrsssygtnlgfwlq
                                                                                                                                                                                                                               IYLRDAVARVEELGIDRSSRMFRHGIJAVAFTSKESVARKIQVMEELGFSRDELLMII
RKAPQLVASSEEKIRQAAEFLKRDVGLEGRYIAHRPVLFLYSLERRLLPRHHILKVLR
MKGLLDCELDYYNTAAMSERKFVRKFVDPYKCHIPGLADAYTSSCAGETANGVASLLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             embryogenesis receptor kinase 1"
/protein_id="BAD37288.1"
/db_xref="G1:51335004"
/translation="MADRRRLILLLVILLCRLAAVLPTSEVEALQGFWAGFAGGNAAF
/translation="MADRRRLILLLVILLGNOSLSGELKPDTWQLQALQSLELYGNSI
SGKIPSELGRLASLQTLDLYLNNFTGEIPNELGNLSKLSNLRLNNNSLSGAIPWSLTT
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SSASSIGTI.I.GGGAAGAAMLFAAPI.YI.FAWWWRRSPHQOFPDI.LEBETPEYHLGQLRR
FTLREI.QVATDNFSQTNLI.CRGGFGKYYRGRI.DIGSI.I.A.I.KRLNBDR.IGTGEROFILAB
VEI.ISMAVHQNI.LIRGOYCMTPFERILVVPYMBNKSLETRIRECSDSQQPLDWPTRRK
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VONGTIGHIPREXLIAGRISDKTDVFGYGVIMLEELISGKREFDLVGLAREBRARYHDW
VKKLLEEDRILEVLIPPRILEIYNGGEGGVREERRILVQIALLCTQESAPSRPRSTVV
TMLEDGIAEHWDAWQRKTIVQASLQGGGCVSEARNDSVANLPPDTLSGPR
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GAGGGGSSKQVLQKCLGANRKNPLVSFL"
                                                                                                                                                                                                             IVGSFDKILKALRMNSSLLGSDLEKVVKPNLELLKQCGMSDFATSFPLYTSRLFTANP
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17652. .17702,18592. .18904))
/gene="P0690H04.6-1"
                                                                                                                                                                                                                                                                                              complement (join(11360. .11924,12422. .12816,12949. .13290, 13368. .13505,13802. .13878,13961. .14032,14104. .14175, 14308. .14451,14834. .14905,14990. .15122,15245. .15747)}
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13368. .13505,13802. .13878,13961. .14032,14104. .14175,
14308. .14451,14834. .14905,14990. .15122,15245. .15408))
C22491(E0081), D24730(R2451), AU173369(R2451), C22490(E0081)
contains full-length cDNA(s): AK104692, AK067095"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="P0690H04.4"
/note="contains full-length cDNA(s): AK065224,AK100258"
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//gene="P0690H04.6-1"
//note="supported by full-length cDNA(8): AK109268"
complement (join(16771. 16955,17062. 17153,17446. 17652. 17702,18592. 18867))
                                         /codon_start=1
/product="mitochondrial transcription termination
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/db_xref="GI:51535005"
                                                                                                    /protein_id="BAD37287.1"
/db_xref="GI:51535003"
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/gene="P0690H04.5"
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and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Immura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kandawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Winyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shizati, T., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shizaki, T., Sogabe, Y., Taqami, M., Taqami-Takada, Y., Taqawa, A., Shizaki, T., Sogabe, Y., and Hayashizaki, Y. Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y. FEATURES J. 2127 /organism="Org	Pred	Qy 153

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Arabidopsis thaliana At2g21940 mRNA for putative shikimate kinase precursor, complete cds, clone: RAFL21-24-A05.
AK118899
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          GlyProAlaValAlaValArgAlaArgGlySerLysProValAlaProLeuArgLeuArg
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EL CDNA: CAP trapper.
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Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Falls Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Falls Genome Sequencing & Analysis Group: Otomo,Y., Iida,Y., Fulls Genome Sequencing & Ishibiki,J., Kawamata,M., Kobayashi,M., Kodayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M., Masuda,M., Miura,J., Mizuno,K., Narikawa,R., Nikukra,J., Oka,M., Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M., Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K. Genome Exploration Research Group in Riken: Adachi,J., Aizawa,K., Akimura,T., Azakawa,T., Carninoi,P., Fukuda,S., Hanapagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayashida,K., Hayashida,K., Hayashida,K., Hayashida,K., Imotani,K., Ishii,Y., Hiraoka,T., Kanagawa,S., Katoh,H., Kawai,J., Kanagawa,J., Kanagawa,S., Katoh,H., Kouda,M., Osto,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakai,K., Nomura,K., Numasaki,A., Ohno,H., Sano,H., Sakai,C., Sakai,K., Sakazume,M., Sano,H., Sakai,C., Sakai,K., Sakazume,M., Tagami,M., Tagami,T., Tagami,Y., Tagami,Y., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K., Yasunishi,A., Tagami,Y., Tomaru,A., Toya,T., Waki,K., Yasunishi,A., Toya,T., Towaru,A., Toya,T., Waki,K., Yasunishi,A., Toya,T., Towaru,A., Toya,T., Waki,K., Yasunishi,A., Toya,T., Toya,T., Toya,T., Waki,K., Yasunishi,A., Toya,T., Toya,T., Toya,T., Wayanishi,F.,
Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizulo, K., Murakami, K., Murata, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, K., Nikura, J., Nishi, K., Nomura, K., Numaaski, R., Ohneda, E., Ohno, M., Ohteuki, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakato, M., Sano, H., Sasaki, D., Sato, K., Satoh, K., Sahbata, K., Shinagawa, A., Sano, H., Sasaki, D., Sato, K., Satoh, K., Sahbata, K., Shinagawa, A., Sano, H., Sasaki, D., Sato, K., Satoh, K., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Taunoda, Y., Uda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.

Direct Submission

L. Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-6602, Japan (E-mail:skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007)

This clone is one of the 28K full-length cDNA clones from japonica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rice.
URL. http://cdna01.dna.affrc.go.jp/cDNA/
NAS Rice Full-Length cDNA Project Team: Kikuchi,S., Satch,K.,
Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
Yamamoto,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arideaccic---cerciciderricececcaacccceccicinescicidescroccaaac 235
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| CCACGCCGCTCTTCCACGGCGAGGGTTCCGGTG---AGGTTCGCGGTGGAGAAGTTCGCT 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MetGluAlaGlyGlyValGlyLeuAlaLeuGlnAlaArgAla---AlaGlyPheGlySer 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Oryza sativa (japonica cultivar-group)"
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
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Query Match:
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RDNETEVLHKLSLMHRLVVSTGGGAVVRPINWRHKGISVWLDVPLEALAKRITTEG
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AEITLEVLIQIENFLKTQKSVVVL"
transit_peptide 123. .320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259 AspAspValSerLysLeuThrProThrAspIleAlaIleGluSerLeuHisLysIleGlu 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                         733
                                                                                                                                                                                                LeuAlaArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeuAspGlnProSer 218
                                                                                                                                                                                                                                                        793
                                                                                                                                                                                                                                                                                                                GlyAspProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnGlnArgGlyAsp 238
                                                                                                                                                                                                                                                                                                                                             239 AlaTyrAlaAsnAlaAspValArgValSerLeuGluGluIleAlaCysLysGlnGlyHis 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spermatophyta, Magnollophyta; eudicotyledons; core eudicots; asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon. [ (bases 1 to 193) Schmid,J., Schaller,A., Leibinger,U., Boll,W. and Amrhein,N. The in-vitro synthesized tomato shikimate kinase precursor is enzymatically active and is imported and processed to the mature
                                                                                                                                                                                                                                                                                                                                                                                                                                                      IleAsnTrpArgTyrMetLysArgGlyLeuSerValTrpLeuAspValProLeuAspAla
                                                                                                                                                                                                                                                        734 TTAGCCCATAGAATCGCTGCTGTTGGAACTGGATTCACGACCACTGCTACACGATGAATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (27-DEC-1991) A. Schaller, Federal Institute of Technology, Institute of Plant Sciences, Sonnegstrasse 5, 8092 Zuerich, SWITZERLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
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L.esculentum mRNA for shikimate kinase precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lycopersicon esculentum (tomato)
Lycopersicon esculentum
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2 (3), 375-383 (1992)
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Schaller, A.
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SOURCE
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REFERENCE
AUTHORS
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TITLE
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JOURNAL
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MEDLINE
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                                                                         Submitted (15-NOV-2002) Motoaki Seki, RIKEN Genomic Sciences Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, 'Jpfgweb.gsc.riken.go.jp, Tel:81-45-503-9625, Rax:81-45-503-9566)
On Dec 5, 2003 this sequence version replaced gi:26452805. An Arabidopsis full-length coll ibrary was constructed essentially set reported previously (Seki et al. (1998) Plant J. 15:707-720; Seki et al. (2002) Science 296:141-145; D.DNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1-B vector (Carninci et al. (2001) Genomics 77:79-90) digested with BamHI and Sall. This clone is in a modified pBluescript vector.
Please visit our web site (http://pfgweb.gsc.riken.go.jp/) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="At2g21940"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              554 GAGATATITIGITICATCACGGAGAGAATITITITAGAGGAAAGGAGACCGAIGCGCITAAG 613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98
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  Nakajima,M., Enju,A., Kamiya,A., Narusaka,M., Carninci,P.,
Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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Matches:
Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Arabidopsis thaliana"
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/gene="At2g21940"
113. .1024
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                          Kawai,J., Hayashiz
Direct Submission
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344 TCAATTGATGAAATCGAGACATTAAAGAATAAAGCAGAAGAAGAAGTTGAAGATATCTAGAT
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                Research,
Direct Submission
Submitted (11-MAY-2004) The Institute for Genomic
Medical Center Drive, Rockville, MD 20850, USA
Location/Qualifiers
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126
35
47
1
                                                 1. .1303

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/mol_type="mRNA"

/db_xref="texon:4081"

/clone="114107R"

/tissue_type="mature green fruit"

/note="TMGHE47"
                                                                    esculentum,
                                                                                                                                                                                  Length:
Matches:
Conservative:
Mismatches:
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BY012339
BY012339.1 G1:47104354
FLI CDNA.
Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Eukaryota, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Lamida; Solanales; Solanaceae; Solanum; Lycopersicon.
(Dasses 1 to 1303)
Kirkness; E.F., Wang, W. and Vazeille, A.
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Matches:
Conservative:
Mismatches:
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/product="shikimate kinase"
/EC_number="2.7.1.71"
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                                                                             2.42e-39
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KEYWORDS SOURCE ORGANISM

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COMMENT

Pred. No.: 8.27e-37 Length: 903 Score: 606.50 Matches: 130 Percent Similarity: 71.37\$ Conservative: 37 Best Local Similarity: 55.56\$ Mismatches: 58 Query Match: 39.74\$ Indels: 9 DB: 8 Gaps: 5	57 ArgleuArgAlaLysLysSerSerGlyGlyHisGluAsnSer	Db 223 CATTCTCCATTTGATGAAGAACAACAGATTTTGAAGAAAAAAGCTGAAGAGTTAAACCG 282 Qy 90 TyrLeuAsnGlyArgCysIleTyrLeuValGlyMetMetGlySerGlyLysSerThrVal 109	Qy 130 GlnAlaValGlyMetDrOSerValAlaGlnIlePheLy8ValHi8SerGluAlaPhePhe 149 Db (403 CAGGCTATGAAGGGAACTTCTGTAGCTGAGATTTTCGGTGAGAGTGTCTTC 462 Qy 150 ArgAspAsnGluSerSerValLeuArgAspLeuSerSerMetArgArgLeuValVal 168	0y 189 SerValTrpLeuAspValProLeuAspAlaLeuAlaArgArg1leAlaLysValGlyThr 208	Db 703 GGTCTTCAACGATGCATGCATGCTGTGTTTTTTTTTTTT	RESULT 15 AK117791 ARADDOPSIS thaliana (thale cress) COURCE ARADIGOPSIS thaliana COURCE ARADIGOPSIS thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. REFERENCE AUTHORS Seki,M., Iida,K., Satou,M., Sakurai,T., Akiyama,K., Ishida,J., NAKAjima,M., Enju,A., Kamiya,A., Narusaka,M., Carninci,P.,
Arabidopsis thaliana (thale cress) Arabidopsis thaliana Macabidopsis thaliana Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermacophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis. 1 (bases 1 to 903) Kim, C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Carninci, P.,	Chada, M.W., Chang, C.H., Dale, J.M., Hayashizak, Y., Hsuah, V.W., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wong, C., Wu, H.C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Davis, R.W., Theologis, A. and	Arabidopsis ORF clones Unpublished 2 (bases 1 to 903) Kim, C.J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Carninci, P., Kim, C.J., Chen, H., Chaug, C. H., Dale, J. M., Hayashizaki, Y., Hsuan, V.W., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J. M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Southwick, A., Tangi, C. C., Toriumi, M., Wongo, C., Wu, H. C., Yamada, K., V. G. Whan S. Shinozaki K. Davis P. W. Thanloris B. and	Ecker, J.R. Direct Submission Submission	icted an , C.J., , C.M., 1., alm,C.J Wu,H.C	Kim,C.J. (SSP/Salk) and SeKi,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Ecker,J.R. (SSP/Salk) contributed equally to this work as PIs. Location/Qualifiers ce 1903 /organism="Arabidopsis thaliana" /mol rype="mcNA" /db_xref="taxon:3702" /chromosone="4" /clone="U60448" /ecotype="Columbia"	/note="This clone is in pUNI 51" 1903 /note="putative shikimate kinase" /codon_start=1 /product="At4g39540" /product="At4g39540" /product="At4g39540" /protein_id="AA06335.1" /db_xref="G1="S950863" /translation="WEAATVORFQYSSWNDLRNFECKPRGSLRYNTORIKEDKRFRVV ALTLDRRADHRARS/SPDRNSSALLETSGLLABPEDEQQLIKKRAEEVRYPINGRSNY INGMGSGKTTVGKINARS/GTTFPFOCDT11EQAMKGTSVABIFBHFGESVFREKETE ALKKLSLMYHQVVVSTGGGAVIRPINWKYMHKGISIMLDVPLEALAHRIAAVGTGSRP LLHDDBSGDTYTAALNRLSTIWDARGEAYTRASARVSLENITLKLGYRSVSDLTPAEI AIEAFEQVQSYLEKEDGMARPDGL"

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PEATURES

CDS

Alignment Scores:

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                                                                  Seki, M., Ilda, K., Satou, M., Sakurai, T., Akiyama, K., Ishida, J., Sakui, M., Ilda, K., Satou, M., Sakurai, T., Akiyama, K., Ishida, J., Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Carninci, P., Nakajima, M., Hayashizaki, Y. and Shinozaki, K.

Kawai, J., Hayashizaki, Y. and Shinozaki, K.

Direct Submission

L. Submitted (125-NOV-2002) Motoaki Seki, RIKEN Genomic Sciences
Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa
230-0045, Japan (B-mail:mseki@gsc.riken.go.jp,
WRL:http://pfgweb.gsc.riken.go.jp, Tel:81-45-503-9625,
Fax:81-45-503-9586)
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al. (1998) Plant J. 15:707-720;
Seki et al. (2002) Science 296:141-145). cDNA cleaved with BamHI
and Xhol was ligated to modified Lambda FLC-1-E vector (Carninci et
al. (2001) Genomics 77:79-90) digested with BamHI and SalI.
This clone is in a modified pBluescript vector.

Please visit our web site (http://pfgweb.gsc.riken.go.jp/) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="putative shikimate kinase"
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AIRAFEQVQSYLEKEDGMARPDGL"
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   Kawai,J., Hayashizaki,Y. and Shinozaki,K.
Arabidopsis thaliana full-length cDNA
Published Only in Database (2002)
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                                                                                                      AlaSerArgProLeuLeu---AspGlnProSerGlyAspProTyrAlaMetAlaPheSer
                           SerValTrpLeuAspValProLeuAspAlaLeuAlaArgArgIleAlaLysValGlyThr
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completed: August 25, 2005, 22:17:38 ne : 5030 secs

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Adk58255 Plant DNA
Adr6836 Cotton on
Adr6836 Cotton on
Ad44520 Bacterial
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Ad867657 Corn seed
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Ad486926 Plant CNA
Ad45821 Bacterial
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Aac36746 Arabidops
Aac41622 Arabidops
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  Aac40184 Arabidops
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AAC40184
AAC4162
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
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    Command line parameters:
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-MODEL=frame+ p2n. model - DEV=xlh
-MODEL=frame+ p2n. model - DEV=xlh
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-NO MAAP - LARGEQUERY - NGG SCORES=0 - WAIT - DSPBLOCK=100 - LONGLOG
-DBV TIMEOUT=120 - WARN TIMEOUT=30 - THREADS=1 - XGAPOP=10 - ACGAPEXT=0.5 - FGAPOP=6
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Aac36026 Arabidops
Aac50026 Arabidops
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                                                                                                                               August 25, 2005, 17:38:27; Search time 610 Seconds (without alignments) 2959.871 Million cell updates/sec
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                    GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                - nucleic search, using frame_plus_p2n model
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Listing first 45 summaries
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Ygapop 10.0 , Ygapext
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19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 20-JUL-1999; 20-JUL-1999; 21-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 23-JUL-1999; 23-JUL-1999; 24-JUL-1999; 25-JUL-1999; 27-JUL-1999; 28-SEP-1999; 28	2-0CT-19
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908 - 0128234P - 908 - 0128234P - 908 - 0128714P - 908 - 0128714P - 908 - 0128714P - 908 - 0120074P - 908 - 0130074P - 908 - 0130074P - 908 - 0130074P - 908 - 0130074P - 908 - 0132484P - 908 - 0132487P - 908 - 0140328 - 908 - 0140328 - 908 - 0140328 - 908 - 014287P -	99US-0144325P. 99US-0144331P.
990S - 0128234P. 990G - 0128714P. 990G - 0128714P. 990G - 0130074P. 990G - 013484P. 990G - 013484P. 990G - 013486P. 990G - 01468P.	0-SD66
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06-APR-1999; 16-APR-1999; 12-APR-1999; 23-APR-1999; 23-APR-1999; 24-APR-1999; 24-APR-1999; 25-APR-1999; 26-APR-1999; 27-APR-1999; 28-APR-1999; 29-APR-1999; 20-APR-1999; 20-APR-1999; 21-APR-1999; 22-APR-1999; 22-APR-1999; 23-APR-1999; 24-APR-1999; 25-APR-1999; 26-APR-1999; 27-APR-1999; 28-APR-1999; 28-APR-1999; 28-APR-1999; 28-APR-1999; 28-APR-1999; 28-APR-1999; 28-APR-1999; 28-APR-1999; 28-APR-1999; 28-APR-1999; 28-APR-1999; 28-APR-1999; 28-APR-1999; 28-APR-1999; 28-APR-1999; 28-APR-1999; 29-AP	19. 19.
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9905-0144333P 9905-0144333P 9905-0144332P 9905-0144332P 9905-0144332P 9905-0144332P 9905-0144332P 9905-0144332P 9905-014432P 9905-0145508P 9905-014593P 9905-014992P 9905-015908P 9905-015908P

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259 AspAspValSerLysLeuThrProThrAspIleAlaIleGluSerLeuHisLysIleGlu 278
                         802 AAAAATGTCTCAGATCTCACACCCAACTGAAATTGCTATCGAGGCCTTCGAGCAAGTCTG 861
                                                                                                                                                                                              pathway;
                                                                                                                                                                                Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic; promoter; termination sequence; ss.
                                                                                                                                                                Arabidopsis thaliana DNA fragment SEQ ID NO: 12278
                                                                                                         BP
                                                                                                                                                                                                                                                                                                 9905-01218025

9905-0123180P

9905-012548P

9905-0125788P

9905-0126784P

9905-01267462P

9905-0128744P

9905-013844P

9905-013091P

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9905-013472P

9905-0137724P
                                                                                                         DNA; 1363
                                                                                                                                              (first entry)
                                                SerPheval 281
                                                           |||||||||
AGCTTTCTA 870
                                                                                                                                                                                                                         Arabidopsis thaliana
                                                                                                         AAC36026 standard;
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05-MAR-1999
25-MAR-1999
25-MAR-1999
01-APR-1999
06-APR-1999
16-APR-1999
16-APR-1999
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30 - APR - 1999;
05 - MAX - 1999;
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14 - MAX - 1999;
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10-JUN-1999;
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128
35
40
0
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Matches:
Conservative:
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Indels:
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99US-0159294P.
99US-0159295P.
99US-0159330P.
99US-0159331P.
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660.00
80.30%
63.05%
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Best Local Similarity:
13-0CT-1999;

13-0CT-1999;

14-0CT-1999;

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18-0CT-1999;

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14 - JUN - 1999; 16 - JUN - 1999; 16 - JUN - 1999; 17 - JUN - 1999; 18 - JUN - 1999; 19 - J	18 - 70N - 1999; 22 - 40M - 1999; 23 - 40M - 1999; 24 - 40M - 1999; 26 - 40M - 1999; 26 - 40M - 1999; 26 - 40M - 1999; 27 - 40M - 1999; 28 - 40M - 1999; 29 - 40M - 1999; 20 - 4	a a a a a a a a a a a a a a a a a a a

	Length: 1363 Matches: 127 Conservative: 35 Mismatches: 0 Gaps: 0
9905-0148319P. 9905-0148341P. 9905-0148341P. 9905-0149368P. 9905-0149368P. 9905-0149722P. 9905-0149722P. 9905-0149723P. 9905-0149922P. 9905-0149923P. 9905-015108P. 9905-01609P. 9905-01609P. 9905-01609P. 9905-01609P. 9905-01609P. 9905-01609P. 9905-01609P. 9905-01609P.	1.11e-53 656.00 79.80% ity: 62.56% 3
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25-MAR-1999,
29-MAR-1999,
01-APR-1999,
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16-APR-1999,
19-APR-1999,
21-APR-1999,
23-APR-1999,
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18-WAY-1999;
18-WAY-1999;
20-WAY-1999;
21-WAY-1999;
25-WAY-1999;
25-WAY-1999;
27-WAY-1999;
28-WAY-1999;
28-WAY-1999;
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10-JUN-1999;
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16-JUN-1999;
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11-MAY-1999;
14-MAY-1999;
14-MAY-1999;
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18-JUN-1999;
18-JUN-1999;
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 GINI1ePheLysValHisSerGluAlaPhePheArgAspAsnGluSerSerValLeuArg 158
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                                                                                                                                                                                                                                     IleabnTrpargTyrMetLybargGlyLeuSerValTrpLeuabpValProLeuabpla 198
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                                                                    ValGlyMetMetGlySerGlyLysSerThrValGlyLysIleMetSerGluValLeuGly
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Gagatatttgttcatcacggagagaattttttagaggaaaggagaccgatgcgcttaag
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                                                                                                                                                                                                                                                                                                                        GlyAspProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnGlnArgGlyAsp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana DNA fragment SEQ ID NO: 63316.
         US-10-660-226-10 (1-305) x AAC36026 (1-1363)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC50026 standard; DNA; 1365 BP
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99US-0123180P.
99US-0123548P.
99US-0125788P.
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AGCTTTCTA 976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
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05-MAR-1999;
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03-AUG-1999;
04-AUG-1999;
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06-AUG-1999;
06-AUG-1999;
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                                                                      280
                                                                                                     977
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                     Arabidopsis thaliana DNA fragment SEQ ID NO: 63328
                                                                                                                                                                                                                                              AAC50029 standard; DNA; 1491 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9905-01231809-9905-01235489-9905-0125649-9905-01262649-9905-01262649-9905-01262649-9905-01280149-9905-01308918-01308918-01308-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-01314499-9905-013143199-9905-013144919-9905-013131249-9905-013131249-9905-013131229-9905-013131229-9905-013131229-9905-013131229-9905-013131229-9905-013131229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312222-9-9905-0131312229-9905-0131312229-9905-0131312229-9905-0131312222-9-9905-0131312222-9-9905-0131312222-9-9905-0131312222-9-9905-0131312222-9-9905-0131312222-9-9905-0131312222-9-9905-0131312222-9-9905-0131312222-9-9905-013131222-9-9905-0131312222-9-9905-0131312222-9-9905-0131312222-9-9905-0131312222-9-9905-0131312222-9-9905-0131312222-9-9905-0131312222-9-9905-0131312222-9-9905-0131312222-9-9905-0131312222-9-9905-0131312222-9-9905-0131312222-9-9905-0131312222-9-9905-0131312222-9-9905-0131312222-9-9905-0131312222-9-9905-0131312222-9-9905-0131312
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99US-0137724P.
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CTA 980
                                                                                                                                    Val 281
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04-JUN-1999;
07-JUN-1999;
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h: 1491 es: 126 rvative: 35	Best Local Similarity; 62.591 Mismatches: 40 Dosey Match: 3 10.500 10.10-660-224-10 (1-36)3 x AAGSGOOD (1-1491) Or 11.500 10.10-660-224-10 (1-36)3 x AAGSGOOD (1-1491) Or 12.10-660-224-10 (1-36)3 x AAGSGOOD (1-1491) Or 12.10-660-224-10 (1-16)1	
rvative:		1491 126 35
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                         230 SerMetLeuAlaGlnGlnArgGlyAspAlaTyrAlaAsnAlaAspValArgValSerLeu
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                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana DNA fragment SEQ ID NO: 27368.
                                                                                                                                    270 AlaileGluSerLeuHisLysileGluSerPheVal 281
                                                                                                                                                     546 ACTCTAGAGGTTCTTATACAAATTCAGAACTTCTTA 581
                                                                                                                                                                                                                              AAC40184 standard; DNA; 1484 BP
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99US-0125788P.
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18-MAY-1999;
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                                                                                                                                                                                                                                                                                                 The invention comprises DNA sequences which confer an altered metabolic characteristic when they are expressed in a plant. The DNA sequences of the invention are useful for producing plants with an altered metabolic characteristic, such as: altered acid metabolism, alcohol metabolism, alcohol metabolism, alcohol metabolism, altered anino acid metabolism, altered ester metabolism, altered anino acid metabolism, altered ester metabolism, altered ester metabolism, altered such estabolism, altered sterol, oxygenated terpene, or isoprenoid metabolism, altered sterol, oxygenated terpene, or metabolism, altered sterol, oxygenated terpene, or metabolism, altered sterol, in The DNA sequences of the invention may be used to provide disease resistance in a plant and gene shuffling or sexual PCR procedures. The present nucleic acid represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 GlyLysileMetSerGluValLeuGlyTyrSerPhePheAspSerAspLysLeuValGlu 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GlnAlaValGlyMetProSerValAlaGlnIlePheLysValHisSerGluAlaPhePhe 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       308
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgAspAsnGluSerSerValLeuArgAspLeuSerSerMetArgArgLeuValValAla 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTTGGTTAGATGTTCCTTTAGATGCTTTGGCCAAGAGAGTTACTGCTGAAGGAACTAAA 368
                                                                                                                                                                                                             Novel genes that confer altered metabolic characteristics in Nicotiana benthamiana plants, useful for altering the levels of metabolites e.g. acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
                                                                                                                                                    Miller BA;
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Jkla V, Larrinua I,
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Reddy AS, S
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                                                                                    (DOWC ) DOW CHEM CO.
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                                                         31-AUG-2001; 2001US-0316471P
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  ||||||| ||||:::::||||||| :::||||||| GAGATGCATACTAGGACGAGGGGGGGGAA 1016
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                                                         ValGlyMetMetGlySerGlyLysSerThrValGlyLysIleMetSerGluValLeuGly
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ThralaSerArgProLeuLeu---AspGlnProSerGlyAspProTyrAlaMetAlaPhe
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09-MAR-1999;

25-MAR-1999;

25-MAR-1999;

06-APR-1999;

06-APR-1999;

16-APR-1999;

16-APR-1999;

23-APR-1999;

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24-MAY-1999;

06-MAY-1999;

06-MAY-1999;

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11-MAY-1999;

11-MAY-1999;
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20-MAY-1999;
21-MAY-1999;
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 188
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PR 02-AUG-1999; 99US-014338P.
PR 04-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-014703P.
PR 05-AUG-1999; 99US-014702P.
PR 05-AUG-1999; 99US-0147102P.
PR 05-AUG-1999; 99US-014710P.
PR 11-AUG-1999; 99US-014712P.
PR 11-AUG-1999; 99US-014712P.
PR 11-AUG-1999; 99US-014972P.
PR 12-AUG-1999; 99US-014972P.
PR 20-AUG-1999; 99US-014972P.
PR 20-AUG-1999; 99US-014972P.
PR 21-AUG-1999; 99US-014972P.
PR 21-AUG-1999; 99US-014972P.
PR 22-AUG-1999; 99US-014972P.
PR 22-AUG-1999; 99US-014972P.
PR 22-AUG-1999; 99US-014972P.
PR 23-AUG-1999; 99US-015546P.
PR 24-SEP-1999; 99US-015549P.
PR
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209 ccacitacarcrostracaracacrocroscarrorrocaaacrosaagrotrorr 268
                                                                                                                                                                                                                               TyrLeuAsnGlyArgCysIleTyrLeuValGlyMetMetGlySerGlyLy8SerThrVal 109
                                                                                                                                                                                                                                                                       GlnAlaValGlyMetProSerValAlaGlnIlePheLysValHisSerGluAlaPhePhe 149
                                                                                                                                                                                                                                                                                                                                       507
                                                                                                                                                                                                                                                                                                                                                           150 ArgAspAsnGluSerSerValLeuArgAspLeuSerSerMet---ArgArgLeuValVal 168
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                                                                                                                                                                                                                                                                                                                                                                                                                        627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    209 AlaSerArgProLeuLeu---AspGlnProSerGlyAspProTyrAlaMetAlaPheSer 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 688 GGTTCAAGACCATTGCTACATGATGATGAGTCAGGGGACACATACACAGCGGCTTTAAAC 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LysLeuSerMetLeuAlaGlnGlnArgGlyAspAlaTyrAlaAsnAlaAspValArgVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ArgleuArgAla------LysLysSerSerGlyGlyHisGluAsnSer------
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| CAGGCTATGAAGGGAACTTCTGTAGCTGAGATATTTGAGCATTTCGGTGAGAGTGTCTTC
                                                                                                                                                                                                                                                                                                                                                                       Hybridisation assay; genetic mapping; gene expression control;
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129
36
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                                                  Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                        Gaps:
                                                                                                                          US-10-660-226-10 (1-305) x AAC36746 (1-1093)
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99US-0161992P.
99US-0161993P.
99US-0162142P.
                                                  4.14e-46
576.50
70.51%
55.13%
37.78%
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                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                                         Alignment Scores:
Pred. No.:
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9905-0140821P.
9905-0141842P.
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31-AUG-1999;
01-SEP-1999;
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protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                               9905-0121825P

9905-0123180P

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9905-0130091P

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9905-0139462P

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9905-0139462P
                                                                                                                        2000EP-00301439
                                        Arabidopsis thaliana
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05-MAX-1999;
06-MAX-1999;
07-MAX-1999;
11-MAX-1999;
14-MAX-1999;
14-MAX-1999;
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21 - 70N - 1999
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05-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
06-APR-1999;
16-APR-1999;
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21-APR-1999;
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21-APR-1999;
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18-MAY-1999;
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27-MAY-1999;
28-MAY-1999;
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23-JUN-1999;
23-JUN-1999;
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30-APR-1999;
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03-JUN-1999;
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10-JUN-1999;
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435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a recombinant polynucleotide comprising any of the 58798 Cotton plant cDNA sequences mentioned in the specification. Also a recombinant polypeptide comprising any of the 58798 amino acid sequences mentioned in the specification and producing a plant having an improved property. Producing a plant having an improved property appared a plant with a recombinant construct comprising a promoter region functional in a plant cell operably joined to a polynucleotide comprising a coding sequence for a polypeptide associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               drought tolerance; plant disease resistance; galactomannan; lignin; plant growth regulator; heat tolerance; herbicide tolerance; homologous recombination; extreme osmotic condition tolerance; pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gossypium
SerValTrpLeuAspValProLeuAspAlaLeuAlaArgArgIleAlaLysValGlyThr
                                                                                                      209 AlaSerArgProLeuLeu---AspGlnProSerGlyAspProTyrAlaMetAlaPheSer
                                                                                                                            436 GGTTCAAGACCATTGCTACATGATGAGTCAGGGGACACATACACAGGGGCTTTAAAC
                                                             376 AGTATTTGGCTTGATGTACCTCTAGAAGCCTTAGCGCATAGAATAGCTGCTGTAGGAACT
                                                                                                                                                                                       496 cerciticaaccartreggargcaccicigaaccaracaraaccaaaccaaacarr
                                                                                                                                                             LysLeuSerMetLeuAlaGlnGlnArgGlyAspAlaTyrAlaAsnAlaAspValArgVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plant; cold tolerance; growth rate; cell cycle pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New recombinant nucleic acid molecules and polypeptides from Go hirsutum, useful for producing plants with improved biological characteristics (e.g. improved plant cold or drought tolerance)
                                                                                                                                                                                                                                                                            AspileAlaileGluSerLeuHisLysIleGluSerPheVal 281
                                                                                                                                                                                                                                                                                             Claim 1; SEQ ID NO 1616; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cotton cDNA sequence, SEQ ID 1616.
                                                                                                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                  ADR60835 standard; cDNA; 1010
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12-DEC-2001; 2001US-00021323.
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                                                                                                                                                                                                                                                                                                                                                                                                                          02-DEC-2004
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                316
                                             189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyLysIleMetSerGluValLeuGlyTyrSerPhePheAspSerAspLysLeuValGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGAAGATTATGGCAAGATCGCTTGGTTATACATTCTTTGATTGTGACACTTTTGATCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlyArgCys1leTyrLeuVal------GlyMetMetGlySerGlyLysSerThrVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ArgAspAsnGluSerSerValleuArgAspleuSerSerMet---ArgArgLeuValVal
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109
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
Matches:
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99US-0159293P
99US-0159294P
99US-0159310P
99US-0159331P
99US-0159631P
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99US-0159631P
99US-0160741P
99US-0160741P
99US-0160767P
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990S-0160815P.
990S-0160981P.
990S-0160981P.
990S-0161404P.
990S-0161404P.
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99US-0161361P.
99US-0161920P.
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99US-0153030P.
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99US-0154039P.
99US-0155139P.
99US-0155139P.
99US-0155659P.
99US-0156458P.
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72.68%
56.19%
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Best Local Similarity:
                            13-SEP-1999;
15-SEP-1999;
16-SEP-1999;
20-SEP-1999;
23-SEP-1999;
24-SEP-1999;
                                                                                                                              28-SEP-1999

29-SEP-1999

06-0CT-1999

06-0CT-1999

07-0CT-1999

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14-0CT-1999

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useful for improving plant cold tolerance, manipulating growth rate in useful for improving plant cold tolerance, manipulating growth rate in clans by modification of the cell cycle pathway, improving plant drought tolerance, providing increased resistance to plant disease, producing galactomannan (or lignin or plant growth regulators), improving plant tolerance, improving plant tolerance to herbicides, increasing the rate of homologous recombination in plants, improving plant tolerance to extreme osmotic conditions or to pathogens or pests, improving yield the rate of homologous recombination in plants, improving yield and/or content, improving yield by modification of photosynthesis, modification of carbohydrate, nitrogen or phosphorus use and/or uptake, or improving yield by providing improved or plant growth and development under at least one stress condition. The polynucleotide and polypeptide may also be used in recombinant DNA constructs, in physical arrays of molecules, as plant breeding markers, continued form part of the princed specification, but was obtained to a Cotton plant cDNA of the invention. NOTE: The sequence data for this patent did not form part of the princed specification, but was obtained in electronic format directly from USPTO at sequence and all S8798 protein sequences were not present.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1010 BP; 286 A; 180 C; 234 G; 310 T; 0 U; 0 Other;
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1010 121 32 61 45 Length: Matches: Conservative: Mismatches: Indels: Gaps: 3.97e-36 473.00 59.53% 47.08% 31.00% Percent Similarity: Best Local Similarity: Query Match: DB:

US-10-660-226-10	-226-10) (1-305) x ADR60835 (1-1010)
ò	30 Th	ThrGlySerLeuArgValAlaAspProAlaGlyProAlaValAlaValArgAlaArgGly 49
qq	214 AC	ACTGGTTCTTTGCGGTTCGATCGGATAGCGAAGCAAGAACACAAG 258
Ġ	50 Se	SerLysProValAlaProLeuArgLeuArgAlaLysLysSerSerGlyGlyHisGlu 68
අු	259 AC	ACCCGGGTGGTTGTTTCGGCCCACTTTCCGGTTCAGACATCTTCCAATCGACATAGATCA 318
ò	89	89
Op	319 GT	GTCTCTTTGGAGGTTTCCTGCTCTTCCTATACGAACTTTTCAGCTTCAACAATGGAAACT 378
È	69	AsnSerHisAsnSerValAspGluAlaLeuLeuLysArgLysSerGluGluVal 87
셤	379 GG	GGCAGCATTCATGCACCTTTTGGTGAAGCTTTAATGTTAAAGAATAAGTCACTAGAGGTT 438
ò	88 Le	LeuPheTyrLeuAsnGlyArgCysIleTyrLeuValGlyMetMetGlySerGlyLysSer 107
qq	439 G	GAGCCATATTTAAATGGGCACAGTATATATCTTGTTGGATTGAGGCTCTGGAAAACT- 497
č	108 T	ThrValGlyLys1leMetSerGluValLeuGlyTyrSerPhePheAspSerAspLysLeu 127
qq	498 AC	
È	128 -1	-ValGluGlnAlaValGlyMetPro135
qa	552 A	::: ::: ::: ::: :::
ò	136 -8	SerValAlaGlnIlePheLysValHisSerGluAlaPhePheArgAspAsnGluSerSe 155
ą	612 G	GTCTGTAGCTGAAATATTTAAGCTTCATGGGGAGAGTTTCTTCAGAAAAAAAGAGACTGA 671
ò	155 r\	rValLeuArgAspLeuSerSerMetArgArgLeuValValAlaThrGlyGlyGlyAlaVa 175
Dp	672 GC	GGTATTGCAGAGGCTTTCTTCACAGAAACAACTTGTTGTTTCTACTGCCGGAGGTGCAGT 731
È	175 11	IleArgProlleAsnTrpArgTyIMetLysArgGlyLeuSerValTrpLeuAspVa 194
qq	732 TC	TGTACAGGATGTGAACTGGGACTATATGCAGAAGAAGGGGATTGTTGTCTGGTTAGATGT 791

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214
              234
                                                           Novel genes that confer altered metabolic characteristics in Nicotiana benthamiana plants, useful for altering the levels of metabolites e.g. acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
                                                                                                                                                                                                                                               Plant DNA sequence which confers altered metabolic characteristic #5640.
                                                                                                                                                                                                                                                                   altered metabolic characteristic; plant; acid metabolism; alcohol metabolism; fatty acid metabolism; branched fatty acid metabolism; alkaloid metabolism; anino acid metabolism; ester metabolism; glyceride metabolism; phenolic metabolism; carbohydrate metabolism; sterol metabolism; terpene metabolism; paptronoid metabolism; alkyne metabolism; hydrocarbon metabolism; ketrone metabolism; alkyne metabolism; disease resistance; gene shuffling; sexual PCR; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blakeslee B, Mccreary DA, Pell RJ;
Reddy AS, Shukla V, Larrinua I, Miller BA;
                                              uAspGlnProSerGlyAspProTyrAlaMetalaPheSerLysLeuSerMetLeuAlaGl
 194 lProteuAspAlaLeuAlaArgArgIleAlaLysValGlyThrAlaSerArgProteuLe
                                                                                                            nGlnArgGlyAspAlaTyrAlaAsnAlaAspValArgValSerLeuGlu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 5640; 2576pp; English.
                                                                                                                                                                        ADK58257 standard; DNA; 660 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DOWC ) DOW CHEM CO. (DOWC ) DOW AGROSCIENCES LLC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-AUG-2002; 2002WO-US027884.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31-AUG-2001; 2001US-0316471P.
                                                                                                                                                                                                                       06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gachotte D,
Crosley R,
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                                                                                                                                                                                                                                                                                                                                                                                     Unidentified.
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                                                                                                                                                                                                 ADK58257;
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The invention comprises DNA sequences which confer an altered metabolic characteristic when they are expressed in a plant. The DNA sequences of the invention are useful for producing plants with an altered metabolic characteristic, such as: altered acid metabolism, alcohol metabolism, fatty acid metabolism, branched fatty acid metabolism, alkaloid or other base metabolism, altered amino acid metabolism, altered ester metabolism, altered glyceride metabolism, altered phenolic metabolism, altered carbohydrate metabolism, altered sterol, oxygenated terpene, or isoprenoid metabolism, alkene or alkyne metabolism, hydrocarbon metabolism, ketone or quinone metabolism. The DNA sequences of the invention may be used to provide disease resistance in a plant and gene shuffling or sexual PCR procedures. The present nucleic acid represents DNA sequence of the invention.

Sequence 660 BP; 194 A; 74 C; 168 G; 224 T; 0 U; 0 Other;

Alignment Scores:

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260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 ATATATCTTGTTGGAATGATGGGTTCTGGAAAAACAACGTGGGAAAGATTTTGTCGGGA 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ValleuGlyTyrSerPhePheAspSerAspLysLeuValGluGlnAlaValGlyMetPro 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTTTAATGAGATAGGGAGGAGGAAG-AAATCATCTAATGGGTTTTTGAGATTATCATCT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SerValAlaGlnIlePheLysValHisSerGluAlaPhePheArgAspAsnGluSerSer 155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37 AspProAlaGlyProAlaValAlaValArgAlaArgGlySerLysProValAlaProLeu
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---TTGAGATGTAATAAGAATTTGGGCACAGGAAATTGGATGGTTTGAGCTTTCTTGT
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|GTACTGAAAGAGTTATCTTTAATGCGTCGGCTGGTTGTTGCC 659
660
91
22
34
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Mismatches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57 ArgieuArgAlaLysLysSerSerGlyGlyHis--
                                                       Matches:
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                                                                                                                                                                                                                                                                                                                                          US-10-660-226-10 (1-305) x ADK58257 (1-660)
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                                        385.50
64.94%
52.30%
25.26%
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                                                                 Percent Similarity:
Best Local Similarity:
Query Match:
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Sequences ABP31028-ABP35561 represent 4534 novel human proteins designated ORF (open reading frame) 1-4534, and sequences ABN75054-Cadesignated ORF (open reading frame) 1-4534, and sequences ABN75054-Cadesignated ORF (open reading frame) 1-4534, and sequences ABN75054-Cadesignated ORF (oplypeptides at least 80% identical to referred to as ORFX) proteins, polynucleotides at least 85% identical to the ORFX nucleic cades sequences, vectors and host cells comprising ORFX caperation or activity, and methods of screening individuals for a predisposition or activity, and methods of screening individuals for a predisposition to an OPFX-associated disorder. The ORFX proteins of the invention have a wide carrivity, and methods of screening individuals for a predisposition to an OFFX-associated disorder. The ORFX proteins of the invention have a wide carrivity, and methods of screening individuals for a predisposition to an OFFX-associated disorder. The ORFX proteins of the invention have a wide carrivity, hasmostatic activity, themostation, cinhibit activity, hasmostatic activity, themostatic activity, hasmostatic activity, themostatic activity, and may also be involved in the determination of bodily characteristics, fertility and behaviour. ORFX proteins, of bodily characteristics, fertility and behaviour. ORFX proteins, content proliferative disorders such as epilepsy and Alzheimer's felace to corgan transplantation, disorders such as psoriasis and benign tumours, corage diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester storage diseases, and infectious diseases caused by virzal, bacterial, corage diseases such as diabetes mellitus, hypothyroidism, and cholesterol ester storage disease, and infection and coloning of homologous course of primers and probes, in the detection of ORFX genomic sequences or transcribts, in the identification and cloning of homologous contents, and in drug screening. The ORFX proteins and bother pathogens. Orfy protein, and in drug screening. The ORFX proteins are seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _{\text{numunogens}} to generate specific antibodies, which are useful in the diagnosis, treatment and monitoring of ORFX-associated diseases
                                                                                                                                                                                                                                                                                                                           Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and disorders related to organ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 G; 85 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 2393; 2508pp; English.
                                              24-MAY-2001; 2001WO-US017076.
                                                                                                24-MAY-2000; 2000US-0206690P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 309 BP; 91 A; 65 C;
                                                                                                                                                                                                Shimkets RA;
                                                                                                                                               (CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                  WPI; 2002-106200/14.
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                                                                                                                                                                                                                                                                                                                                                                                                         transplantation
29-NOV-2001.
                                                                                                                                                                                                   Leach MD,
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AlaArgArg1leAlaLysValGlyThrAlaSerArgProLeuLeuAspG1nProSerGly 219

200

WO200190366-A2

309 74 113 0

Length:
Matches:
Conservative:
Mismatches:

3.17e-27 374.00 85.29% 72.55% 24.51%

Alignment Scores:

Indels: Gaps:

Similarity:

Percent Similarity: Best Local Similari

Query Match:

US-10-660-226-10 (1-305) x ABN79354 (1-309)

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DNA sequence of the invention.
                                                       Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention comprises DNA sequences which confer an altered metabolic characteristic when they are expressed in a plant. The DNA sequences of the invention are useful for producing plants with an altered metabolic characteristic, such as: altered acid metabolism, alcohol metabolism, fatty acid metabolism, altered amino acid metabolism, altered ester metabolism, altered setten metabolism, altered setten metabolism, altered setten metabolism, altered setten, oxygenated terpene, or isoprenoid metabolism, altered sterol, oxygenated terpene, or metabolism, altered setten metabolism, altered setten metabolism, altered setten metabolism, bydrocarbon metabolism, ketone or quinone metabolism. The DNA sequences of the invention may be used to provide disease resistence in a plant and gene shuffling or sexual PCR procedures. The present nucleic acid represents a
                                                                                                             240
                                                                                                                                                                    300
                                                                                                                                         279
                                           GCAAGAAGAATTGCTGCTGTAGGAACCGCGTCTCGACCACTCTTGCATCAGGAATCCGGT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel genes that confer altered metabolic characteristics in Nicotiana benthamiana plants, useful for altering the levels of metabolites e.g. acids, fatty acids, amino acids, carbohydrates, hydrocarbons and sterols.
                                                                                                                                                                                                                                                                                                                                                                  Plant DNA sequence which confers altered metabolic characteristic #5638.
                                                                                                                                                                                                                                                                                                                                                                                                           alcohol metabolism, fatty acid metabolism;
branched fatty acid metabolism; alkaloid metabolism;
amino acid metabolism; ester metabolism; glyceride metabolism;
phenolic metabolism; carbohydratte metabolism; sterol metabolism;
terpene metabolism; isoprenoid metabolism; alkene metabolism;
alkyne metabolism; hydrocarbon metabolism; ketone metabolism;
quinone metabolism; disease resistance; gene shuffling; sexual PCR; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BA;
                                                                                                           181 TATGCTAATGCTGATGCCAGAGTTTCACTTGAACATATTGCATTAAAACAAGGCCATAAT
                                                                                                                                                       241 GATGTCACTATACTTACACCTAGTACCATCGCCATTGAGGCATTGCTAAAGATGGGAAGT
                           AspproTyralaMetAlaPheSerLysLeuSerMetLeuAlaGlnGlnArgGlyAspAla
                                                                                 TyrAlaAsnAlaAspValArgValSerLeuGluGluIleAlaCysLysGlnGlyHisAsp
                                                                                                                                       AspvalSerLysLeuThrProThrAspIleAlaIleGluSerLeuHisLysIleGluSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Miller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ' DA, Pell RJ;
Larrinua I, M
                                                                                                                                                                                                                                                                                                                                                                                              metabolic characteristic; plant; acid metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3, Mccreary
Shukla V, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 5638; 2576pp; English.
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(DOWC ) DOW AGROSCIENCES LLC.
                                                                                                                                                                                                                                                                                  ADK58255 standard; DNA; 329
                                                                                                                                                                                                                                                                                                                                        (first entry)
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Crosley R,
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                                                                                                                                                                                                PheVal 281
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Oriedo JVB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              drought tolerance; plant disease resistance; galactomannan; lignin; plant growth regulator; heat tolerance; plant growth regulator; ketteme osmotic condition tolerance; homologous recombination; extreme osmotic condition tolerance; pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
                                                                                                                                                                                                                                                                                                                        LysileMetSerGluValLeuGlyTyrSerPhePheAspSerAspLysLeuValGluGln
                                                                                                                                                                                                                                          LeuAsnGlyArgCysIleTyrLeuValGlyMetMetGlySerGlyLysSerThrValGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plant; cold tolerance; growth rate; cell cycle pathway;
G; 96 T; 0 U; 0 Other;
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18
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Conservative:
Mismatches:
Indels:
                                                           Length:
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93 A; 52 C; 88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-JAN-2004; 2004US-00767795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAY-2001; 2001US-00849529.
12-DEC-2001; 2001US-00021323.
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                                                         1.31e-26
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66.35%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (KOVA/) KOVALIC D K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-667718/65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gossypium hirsutum.
                                                                                                                  Best Local Similarity:
Query Match:
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  BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CAOY/) CAO Y.
                                                                                                     Percent Similarity:
Sequence 329
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New recombinant nucleic acid molecules and polypeptides from Gossypium hirsutum, useful for producing plants with improved biological characteristics (e.g. improved plant cold or drought tolerance).
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ID NO 1617; 14pp; English. Claim

The invention relates to a recombinant polymucleotide comprising any of the 58798 Cotton plant cDNA sequences mentioned in the specification.

Also a recombinant polypeptide comprising any of the 58798 amino acid sequences mentioned in the specification and producing a plant having an improved property.

Comprises transforming a plant with a recombinant construct comprising a promoter region functional in a plant cell operably joined to a promoter region functional in a plant cell operably joined to a polypeptide associated with the property, and growing the transformed plant. The polypeptide is constituted in miproving plant cold tolerance for a polypeptide associated useful for improving plant cold tolerance, manipulating growth rate in plant tolerance, providing increased resistance to plant disease.

Concursing galactomannan (or lignin or plant growth regulators), improving plant tolerance to reach of the cell cycle pathway, improving plant tolerance to extreme osmocic conditions or plant growth regulators), improving teld by modification of photosynthesis, modifying seed oil or protein yield by modification of photosynthesis, modification of exception improved plant growth and development under at least one stress condition. The conformation in physical arrays of molecules, as plant breeding markers, or in computer-based storage and analysis systems. The present sequence is a cotton plant cDNA of the printed specification, but was obtained constructs, in physical arrays of molecules, as plant breeding markers, or patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence data for this constructed assembles are available, the remaining 5231 polynucleotide sequences were available, the remaining 52213 polynucleotides and all 58798 protein sequences were not present.

Sequence 614 BP; 170 A; 98 C; 154 G; 192 T; 0 U; 0 Other;

614 80 21 34 1 Length:
Matches:
Conservative:
Mismatches:
Indels: Gaps: 1.04e-25 362.50 73.72% 58.39% Percent Similarity: Best Local Similarity: Alignment Scores: Query Match

Claim 1; SEQ ID NO 7361; 34pp; English.

US-10-660-226-10 (1-305) x ADR60836 (1-614)

169 AlaThrGlyGlyGlyAlaVallleArgProlleAsnTrpArgTyrMet---LysArgGly 187 PheArgAspAsnGluSerSerValLeuArgAspLeuSerSerMetArgArgLeuValVal 168 61 TCTACTGGCGGAGGTGCAGTTGTACGGGATGTGAACTGGGACTATATGCAGAAGAAGGGG 120 Acrearricricicecerririscarrargaacaresceáricecráracaassecrirraaaa 240 228 LysieuSerMetLeuAlaGlnGlnArgGlyAspAlaTyrAlaAsnAlaAspValArgVal 247 cescifercitaccititicas concades de carana a a transcita a a concidenta a concesión de concesión SerLeu-GluGluileAlaCysLysGlnGlyHisAspAspValSerLysLeuThrProTh 267 9 ThralaSerArgProLeuLeuAspGlnProSerGlyAspProTyrAlaMetAlaPheSer LeuSerValTrpLeuAspValProLeuAspAlaLeuAlaArgArgIleAlaLy8ValGly 149 188 121 181 208 248 g g g ò 셤 ò ò 음 ò ò ò

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Cotton; plant; EST; expressed sequence tag; transgenic plant; androecium; variety Nucotton33B; library LIB382B; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss.
                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular
                                                                                                                 Cotton androecium tissue EST Clone ID: LIB3828-016-Q1-N6-D8, SEQ:7361.
           rAspileAlaileGluSerLeuHisLysileGluSerPheValileGlu
                                                                                                                                                                                                                                                                                                                                  Ziegler TE;
                                                                                                                                                                                                                                                                                                                                  Fincher KL,
                                                         BP.
                                                                                                                                                                                                                                             12-DEC-2001; 2001US-00021323.
                                                                                                                                                                                                                                                              14-DEC-2000; 2000US-0255619P.
                                                        ACN52580 standard; cDNA; 573
                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                  Deikman J, Feng PCC,
                                                                                                                                                                                                                                                                                (DEIK/) DEIKMAN J.
(FENG/) FENG P C C.
(FINC/) FINCHER K L.
(ZIEG/) ZIEGLER T E.
                                                                                                                                                                                                                                                                                                                                                     WPI; 2004-479808/45.
                                                                                                                                                                                   Gossypium hirsutum.
                                                                                                                                                                                                                                                                                                                                                                                                     tags to map genes.
                                                                                                                                                                                                      US2004123340-A1.
                                                                                               02-DEC-2004
                                                                                                                                                                                                                         24-JUN-2004.
                                                                             ACN52580;
 267
                   361
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The invention relates to 17880 cotton expressed sequence tags (ESTB;
ACN45220-ACN63099). The ESTB were isolated from cDNA libraries generated
CC from primed seeds from variety DBSOB, mature seeds from
variety Coker 312 Boswell 96 Field, and androecium tissue, gynoecium
tissue, developing fibres, carpel walls and septa from variety
CC welloping fibres, carpel walls and septa from variety
CC broteins or their fragments encoded by nucleic acid molecules of the
invention, and to transformed plants having a mucleic acid construct
CC comprising a nucleic acid of the invention. The cotton ESTB are useful as
CC comprising a nucleic acid of the invention. The cotton ESTB are useful
CC comprising a nucleic acid of the invention and to determining whether genes are
CC comprising a nucleic acid of the invention. The cotton ESTB are useful
CC comprising a nucleic acid of the invention and to determining whether genes are
CC comprising a nucleic acid anily. The nucleic acid molecules may be
CC members of a particular gene family. The nucleic acid molecules are
CC seed for isolating a variety of agronomically significant genes
CC associated with plant growth, quality, yield, and could also serve as
CC links in metabolic and catabolic pathways. The nucleic acid molecules are
CC during seed germination or that may be used to mitigate stresses encountered
CC during seed germination. The ESTS additionally enable the acquisition of
CC during seed germination or that may be used to mitigate stresses encountered
CC during seed germination or the ESTS additionally enable the acquisition of molecular markers useful for and also permits the acquisition of molecular markers useful for detecting the expression level or pattern of a protein or mRNA and for
CC detecting the expression level or pattern of a protein or mRNA and for
CC detecting the presence or quantity of a protein by tissue printing. The
CC resequence requence represents a special count of the printed
CC sequence data for this patent did not form part of the printed

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specification, but was obtained in electronic format directly from the US patent office at segdata.uspto.gov/sequence.html?DocID=US20040123340
                                                                                                                                388 ACAAAGGCTTTAAAACGTCTGTCTTACCTTTTGGAGCAGAGGGGTAAAAATTATGCTAAA 329
                                                                                                                                                                                                                                                                             223 AlaMetAlaPheSerLysLeuSerMetLeuAlaGlnGlnArgGlyAspAlaTyrAlaAsn 242
                          Sequence 573 BP; 183 A; 138 C; 86 G; 166 T; 0 U; 0 Other;
                                                    573
73
18
29
1
                                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                   2.68e-24
347.50
75.21%
60.33%
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Query Match:
DB:
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                                          Alignment Scores:
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Sequence 795, App Sequence 86, Appl Sequence 1574, Ap Sequence 2, Appli Sequence 1, Appli

Sequence 1141, Ap Sequence 21, Appl Sequence 26, Appl

Sequence 6367, Apple Sequence 1, Appli Sequence 1, Appli Sequence 173, Apple Sequence 166, Apple Sequence 167, Apple Sequence 177, Apple Sequence 37, Apple Sequence 37, Apple Sequence 280, Apple Sequence 11379, Apple Sequence 11279, Apple Sequence 11279, Apple Sequence 11279, Apple Sequence 1235, A

Sequence 4775, Ap Sequence 1235, Ap Sequence 9022, Ap Sequence 2, Appli

Sequence 949, App Sequence 985, App

3, Appli 3, Appli

Sequence Sequence Sequence

us-10-660-226-10.rni

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Second 1677 Application US/09540236

Setent No. 6673910
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAFTILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT PAPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITICATIGAAGAGGIGAIGGICGAAAAGCAGGIAAIGCCIIAICAAAACAACIACCIG 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LeuLeuLeuLysArg-----LysSerGluGluValLeuPheTyrLeuAsnGly-ArgCy
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3 US-09-134-000-1574
4 US-09-134-000-1574
5 3 US-09-134-000-1574
6 US-09-134-000-1574
7 US-09-103-840A-1
7 US-09-043-61A-1141
7 US-09-043-61A-1141
7 US-09-043-039A-6367
7 US-09-043-185A-1
7 US-09-134-185A-1
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7 US-09-135-665-1
7 US-09-135-665-1
7 US-09-102-540-1143
7 US-09-102-540-1143
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US-09-540-236-167
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Pred. No.:
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-MODEL=frame+ p2n.model -DEV=xlh
-O=/cgn2_1/USPTO_epool/US10660226/runat_25082005_I10428_28555/app_query.fasta_1.455
-O=/cgn2_1/USPTO_epool/US10660226/runat_25082005_I10428_28555/app_query.fasta_1.455
-DB=168046_Patents NA -QFMT=fastap -SUFFTX=ni -MINMATGH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=Dits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=Eptt -THR MAX=100 -THR MINS 0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NOFM=ext -HEAPSIZE=500 -MINLEN=0 -WAXLEN=-200000000
-USER=US10660226_@CGN 1 1 69 @runat_25082005_110428_28555 -NCPU=6 -ICPU=3
-NO MAAP -LARGEQUERY -NGG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DBV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Sequence 2023, Ap
Sequence 3641, App
Sequence 1, Appli
Sequence 1, Appli
Sequence 2510, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 16393, A
Sequence 216, Ap
                                                                                                                                         August 25, 2005, 20:28:39; Search time 203 Seconds (without alignments) 2458.445 Million cell updates/sec
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-596-002-11
US-09-328-352-2023
US-09-489-035A-3641
4 US-09-557-884-1
4 US-09-557-884-1
4 US-09-557-888-1
US-09-730-988-1
US-09-730-988-1
US-09-252-991A-16593
US-09-252-991A-16593
US-09-252-991A-16502
US-09-107-532A-2146
US-09-583-110-886
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Maximum Match 100%
Listing first 45 summaries
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Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext (
Delop 6.0 , Delext
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Result Š.

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Carguence 2023, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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                                                                                                   10794 CTTTCATTGAAGAGGTGATGGTCGAAAAAGCAGGTAATGCCTTATCAAAACAACTACCTG 10853
                                                                                                                                                                                                                                                                                                             10914 AACATTTGGGGCGTAATTTCATTGATTGCGATTGGTATATCGTTGATCAAACGGGT---G 10970
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                                                                                                                                                    s-ileTyrLeuValGlyMetMetGlySerGlyLysSerThrValGlyLysIleMetSerG 115
                                                                                                                                                                                                                                                          115 luValLeuGlyTyrSerPhePheAspSerAspLysLeuValGluGlnAlaValGlyMetP 135
                                                                                                                                                                                                                                                                                                                                                                135 roSerValAlaGlnIlePheLysValHisSerGluAlaPhePheArgAspAsnGluSerS 155
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                                                LeuLeuLysArg-----LysSerGluGluValLeuPheTyrLeuAsnGly-ArgCy
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Matches:
Conservative:
US-10-660-226-10 (1-305) x US-09-596-002-11 (1-14335)
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US-09-328-352-2023
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LENGTH: 603
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231 MetLeuAlaGlnGlnArgGlyAspAlaTyrAlaAsn---AlaAspValArgValSerLeu 249
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                                                                                                                                                                                                                                                                                              ----GTGCTGGAA 483
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         391 GAAACTACGATCGAGAAGCAGTTGGCCCGTACGCAGCGC-----GATAAAAGCGTCCT
                                                                           174 AlaVal --- IleArgProlleAsnTrpArgTyrMetLysArgGlyLeuSerValTrpLeu
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APPLICANT: Fleischmann et al.
ATLE OF INVENTION: The Nuclectide sequence of
the Haemophilus influenzae Rd
Thereof, and Uses Thereof
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                              445 TIGCTACAAGICGAIGCGCCGCCTCGIGAA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          568 GCGAACCAGATTATTCATATGCTGGAAAGC 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS V6.22
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270 AlalleGluSerLeuHisLysIleGluSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1830121 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 301-309-8504
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STRANDEDNESS: double
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SEQUENCE CHARACTERISTICS:
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STATE: MD
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ZIP: 20850
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US-09-557-884-1
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 3641
LENGTH: 603
                                                                                                                                                                 ValleuArgAspleuSerSerMetArgArgleuValValAlaThrGlyGlyGlyAlaVal 175
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154 CTATTAGGGCGTGAATTTTTAGATAGTGATCATGAAATTGAGCGCAAGACAGGG---GCC
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Matches:
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Mismatches:
Indels:
Gaps:
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                                                                                               US-10-660-226-10 (1-305) x US-09-328-352-2023 (1-603)
             Mismatches:
                             Indels:
Gaps:
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Best Local Similarity: 42,50%
Ouerv Match: 14.55%
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                           Query Match:
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|GACATCACT----TTGCCAACGAT 222071
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Matches:
Conservative:
Mismatches:
                                                                                                                                                              NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,302
REFERNCE/DOCKET NUMBER: PB186F1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels:
                                      PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
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8-09-543-681A-2510
; Sequence 2510, Application US/09543681A
; Patent No. 6605709
                                                                                                                                                                                                                                                                                                                              LENGTH: 1830121 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
    FILING DATE: 23-Aug-2000
CLASSIFICATION: <Unknown>
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214.00
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14.02$
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                              ---GCGGATATTAGCTGGATTTTTGGAAGGCGAAGACGCTTCCGAAAACGTGAA
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                     Matches:
Conservative:
Mismatches:
Indels:
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CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09643990A
Patent No. 6528289
GENERAL INFORMATION:
APPLICANT: RObert D. Fleischmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mark D. Adams
Owen White
Hamilton O. Smith
J. Craig Venter
    1.18e-08
                     214.00
54.55%
33.52%
14.02%
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                                                              Best Local Similarity:
                                          Percent Similarity:
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US-09-643-990A-1
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us-10-660-226-10.rni

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Sequence 16393, Application US/09252991A
Sequence 16393, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILLE REPERRENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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                                             BACTERIAL SYMBIONT OF APHIDS
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Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                          Length:
Matches:
                         APPLICANT: SAKAKI, YOSHIYUKI
TITLE OF INVENTION: GENOME DNA OF BACTERIAL
FILE REFREENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: JP2000-107160
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
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            HATTORI, MASAHIRA
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                                                                                                                                                                                                                                   ORGANISM: Buchnera
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Best Local Similarity:
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US-09-252-991A-16393
                                                                                                                                                                                 SEQ ID NO 1
LENGTH: 640681
                                                                                                                                                                                                                                                                                        Alignment Scores:
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TITLE OF INVENTION: UNCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT PILIGN DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR PILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
LEMBER OF SEQ ID NOS: 8344
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Matches:
Conservative:
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Patent No. 6632935
GENERAL INFORMATION:
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212.50
50.27%
34.22%
13.93%
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US-09-543-681A-2510
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                   TYPE: DNA ORGANISM:
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241 AlaAsn---AlaAspValArgValSerLeuGluGluIleAlaCysLysGlnGlyHisAsp 259
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Mismatches:
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FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
FILOR APPLICATION NUMBER: US 60/074,788
FILOR APPLICATION NUMBER: US 60/094,190
FRIOR APPLICATION NUMBER: US 60/094,190
FRIOR FILING DATE: 1998-07-27
FRIOR FILING DATE: 1998-07-27
SEQ ID NO 16202
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US-09-107-532A-2146
; Sequence 2146, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
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205.50
49.29%
32.70%
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Best Local Similarity:
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Pred. No.:
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                                                                                                                                                                                                                                                555
69
35
71
37
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                                                                                                                                                                                                                                                                                                                                                            Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              260 AspValSerLysLeuThrProThrAspIleAla 270
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels:
     PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FLILNG DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142 SEQ ID NO 16393
                                                                                                                                                                                                                           Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                          6.04e-13
205.50
49.29%
32.70%
13.47%
                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-252-991A-16202/c
                                                                                                                                                                                                                                                     US-09-252-991A-16393
                                                                                                                                                                                                                                                                                                         Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                           ORGANISM:
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                                                                                                                                                                                                     DNA
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                                                                                                                                                                                                                                                                                                                                                              Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            셤
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576 69 35 71 37

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Sequence 886. Application US/09583110
| Patent No. 6699703
| Patent No. 6699703
| APPLICANT: Lynn Doucette-Stamm et al. |
| APPLICANT: Lynn Doucette-Stamm et al. |
| TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus |
| TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus |
| TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus |
| FILE REFERENCE: PATHOD-07A |
| CURRENT APPLICATION NUMBER: US/09/583,110 |
| PRIOR APPLICATION NUMBER: US 60/085,131 |
| PRIOR APPLICATION NUMBER: US 60/085,131 |
| PRIOR PILING DATE: 1998-06-30 |
| PRIOR PILING DATE: 1998-05-12 |
| PRIOR PILING DATE: 1998-05-12 |
| PRIOR PILING DATE: 1997-07-02 |
| NUMBER OF SEQ ID NOS: 5322 |
| SEQ ID NO 886 |
| LENGTH: 477
                                                       271 CAAAGTGCAGAAAATCGGCGTTTTTTAAAAACACAGCCGATTGTTCTTTACTTAGAGGCA 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 ArgAspLeuSerSerMetArgArgLeuValValAlaThrGlyGlyGlyGlyAlaValIleArg 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        178 GCTGATTTACTACAAACAGACCAA---GTCGTGTCAACTGGAGGAGGAGTGGTTATTTCT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        118 GlyTyrSerPhePheAspSerAspLysLeuValGluGlnAlaValGlyMetProSerVal 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 AlaGlnIlePheLysValHisSerGluAlaPhePheArgAspAsnGluSerSerValLeu 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 GCGAATTTTTCGCTGAAAGGGAGAGAGCCTTTCGTCAGGTAGAATCAGAAGTCCTA 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    176 IleArgProIleAsnTrpArgTyrMetLys---ArgGlyLeuSerValTrpLeuAspVal 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                197 AspAlaLeuAlaArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeuAspGln 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              355 AATAGCAAGGAA---------GAACTAGTAGCTATTTTCAAGAAGA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               237 GlyAspAlaTyrAlaAsnAlaAspValArgValSerLeuGluGluIleAlaCysLysGln 256
                                                                                                                                                          331 GAAGCGGACTGTCTAGTTGTATCCAACAAGATGAAACGTCTATTCGACCTTTA 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98 LeuValGlyMetMetGlySerGlyLysSerThrValGlyLysIleMetSerGluValLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |||:::||| ||||||::|||
13 TTATTAGGGTTTATGGGGGCTGGAAAATCGACTATTGCAAGA------GGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 GACACTAATTACCTTGATATGGATGCTCTGATTGAGAAGCGCCTAGGTATG---TCCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          178 ProlleAsnTrpArgTyrMetLysArgGlyLeu---SerValTrpLeuAspValProLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       217 ProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnGlnArg
                                                                                                                195 ProLeuAspAlaLeuAlaArgArgIleAlaLysValGlyThrAlaSerArgProLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        477
62
27
63
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Mismatches:
Indels:
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Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Streptococcus pneumoniae US-09-583-110-886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.45e-10
179.00
50.00%
34.83%
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Best Local Similarity:
Query Match:
DB:
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APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IleTyrLeuValGlyMetMetGlySerGlyLysSerThrValGlyLysIleMetSerGlu 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SerValAlaGlnIlePheLysValHisSerGluAlaPhePheArgAspAsnGluSerSer 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||:::|||:::
| TCGATTGCCGAATATTTTCACTATTACGGTGAAAAAGGCTTTCGAAAAGTGGAGTCAGAT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 ValLeuGlyTyrSerPhePheAspSerAspLysLeuValGluGlnAlaValGlyMetPro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  537
29
44
43
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                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
Matches:
Conservative:
Mismatches:
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                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMFUTER: PC
COMPUTER: PC
COMPUTER: CD/ROM ISO9660
COMFUTER: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/085,598
RILING DATE: JUPY 2, 1997
ATTORNEY/AGENT INFRMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...537
SEQUENCE DESCRIPTION: SEQ ID NO: 2146:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Enterococcus faecium
                                                                                                                                 STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 2146:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: circular
MOLECTLE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 537 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                     SEQUENCES: 7310
                                                                                                                                                     CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8.19e-11
185.50
61.34%
36.97%
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-107-532A-2146
                                                                     NUMBER OF
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DB:
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Sequence 86, Application US/08961527

Patent No. 6420135

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITT: Rockville
STATE: Maryland
COUNTRY: USA
                118 GlyTyrSerPhePheAspSerAspLysLeuValGluGlnAlaValGlyMetProSerVal 137
                                              64 GACACTAATTACCTTGATATGGATGCTCTGATTGAGAAGCGCCTAGGTATG---TCCATT 120
                                                                                                         AlaGlnIlePheLysValHisSerGluAlaPhePheArgAspAsnGluSerSerValLeu 157
                                                                                                                                                     121 GCGAATTTTTTCGCTGAAAGGGAGAAGAGCCTTTCGTCAGGTAGAATCAGAAGTCCTA 180
                                                                                                                                                                                                 158 ArgAspLeuSerSerMetArgArgLeuValValAlaThrGlyGlyGlyAlaValIleArg 177
                                                                                                                                                                                                                        178 ProlleAsnTrpArgTyrMetLysArgGlyLeu---SerValTrpLeuAspValProLeu 196
                                                                                                                                                                                                                                                                                                                 |||
238 CAGAGAAATCGTGACTTACTCAAGACTAATACAGATAACATCTACCTGAAAGCAGATTTT 297
                                                                                                                                                                                                                                                                                                                                                                           197 AspAlaLeuAlaArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeuAspGln 216
                                                                                                                                                                                                                                                                                                                                                                                                                    298 GAAACCCTCTACCAACGTATCGCAGCTGATAAGGACAATCAGCGACCGCTTTTTCTAAAT 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          358 AATAGCAAGGAA------GAACTÁGTAGCTATTTTCAÁGAAÁGÁ 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     237 GlyAspAlaTyrAlaAsnAlaAspValArgValSerLeuGluGluIleAlaCysLysGln 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            217 ProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnGlnArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          257 GlyHisAspAspValSerLysLeuThrProThrAspIleAlalleGluSerLeu 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: Z0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS VERSION 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/961,527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 9834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 19390 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                   RESULT 1.3
US-09-107-433-795
US-09-107-433-795
Sequence 795, Application US/09107433
Fatent No. 6800744
FAPELICANTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
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                                         257 GlyHisAspAspValSerLysLeuThrProThrAspIleAlaIleGluSerLeu 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION UNIBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Atiniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: GTC-011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels:
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LOCATION: (B) LOCATION 1...480
SEQUENCE DESCRIPTION: SEQ ID NO: 795:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                  100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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TYPE: nucleic acid
STRANDEDNESS: double
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INFORMATION FOR SEQ ID NO: 795:
SEQUENCE CHARACTERISTICS:
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COUNTRY: USA
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CORRESPONDENCE ADDRESS:
  394 CAGGCTTGGTAT-
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ORIGINAL SOURCE:
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Job time : 762 secs
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APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION:
NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR FILING DATE: 1997-08-15
PRIOR FILING DATE: 1997-08-15
                                                                                                                                                                                                                                                                                157
                                                                                                                                                                                                                        118 GlyTyrSerPhePheAspSerAspLysLeuValGluGlnAlaValGlyMetProSerVal 137
                                                                                                                                                                                                                                                                                                                                    158 ArgAspieuSerSerMetArgArgLeuValValAlaThrGlyGlyGlyAlaValIleArg 177
                                                                                                                                                                                                                                                                                                                                                                                          178 ProlleAsnTrpArgTyrMetLysArgGlyLeu---SerValTrpLeuAspValProLeu 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                197 AspAlaLeuAlaArgArgileAlaLysValGlyThrAlaSerArgProLeuLeuAspGln 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     217 ProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnGlnArg 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          237 GlyAspAlaTyrAlaAsnAlaAspValArgValSerLeuGluGluIleAlaCysLysGln 256
                                                                                                                                                               LeuValGlyMetMetGlySerGlyLysSerThrValGlyLysIleMetSerGluValLeu 117
                                                                                                                                                                                                                                                                              138 AlaGlnIlePheLy8ValHisSerGluAlaPhePheArgAspAsnGluSerSerValLeu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Enterococcus faecalis
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SEQ ID NO 1574
LENGTH: 513
                                      1.36e-07
177.00
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                                                                                Best Local Similarity:
Query Match:
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US-09-134-000C-1574
                                                                  Percent Similarity:
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                                                                                                                                                                                                       96 IleTyrLeuValGlyMetMetGlySerGlyLysSerThrValGlyLysIleMetSerGlu 115
                                                                                                                                                                                                                                                                                                                                                                                                              76 AAACTGAAGATGCCTCATCTTGATTTAGATACAGCGTTAATTGAAAAAATAGGACGC--- 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   195 ProLeuAspAlaLeuAlaArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeu 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   310 ACACCAGAAGAGCTGTTAAAAGAATCACAGAAGATACTGAAAACCAACGGCCCTTAGCT 369
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                                                                                                                                                                                                                                              16 ATTGTTTTAATTGGTTTCATGGGTGCGGGTAAAACAACTATCGGCCAAAGTTTGGCCAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 ValleuGlyTyrSerPhePheAspSerAspLysLeuValGluGlnAlaValGlyMetPro
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Mismatches:
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-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/cgn2 1/USPTO_spool/US10660226/runat_25082005_I10428_28579/app_query.fasta_1.455
-Q=/cgn2 1/USPTO_spool/US10660226/runat_25082005_I10428_28579/app_query.fasta_1.455
-DB=Published Applications NA -QEMT=fastap -SUPFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -ENN=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=0
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=cto -NORM=ext -HEAPSTZE=500 -NINLEN-0
-MAXLEN=2000000000 -USER=US10660226 @CGN 1 1 480 @runat_25082005_I10428_28579
-NCPUG=6 -ICPUG=3 -NO MAAP -LARGEQUERY -NGS GCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOTT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPDEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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(cgn2_6/ptodata1/lpubpna/USO9_PUBCOMB.seq:*

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(cgn2_6/ptodata1/lpubp
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                             - nucleic search, using frame_plus_p2n model
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
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6610, Ap 2317, Ap 11266, A 1680, Ap 1616, Ap 25738, A

Sequence 1 Sequence 2 Sequence 3 Sequence 6 Sequence 6 Sequence 6

523, App 137299, 29612, A

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5640, Ap 70060, A 8601, Ap 2538, Ap 1617, App 7361, Ap 11365, A

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2340, Ap 57, Appl 29872, A 70058, A 68871, A 19, Appl 25, Appl 16473, 7 4532, A score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Sequence US-10-425-115-16472
US-10-425-115-16472
US-10-425-114-35273
US-10-425-114-35273
US-10-425-114-35273
US-10-425-115-16474
US-10-767-701-13420
US-10-425-115-16473
US-10-425-115-16473
US-10-425-115-68871
US-10-660-226-19
US-10-660-226-19
US-10-660-226-19
US-10-425-115-68871
US-10-425-115-68871
US-10-425-115-16469
US-10-425-115-16469
US-10-425-115-16469
US-10-425-115-16469
US-10-425-116-2917
US-10-424-599-70660
US-10-424-599-70660
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US-10-424-599-70660
US-10-424-599-70660
US-10-424-599-70660
US-10-660-226-21
US-10-707-795-1617 SUMMARIES

ALIGNMENTS

APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Sovoal: C. David K.
APPLICANT: Soreen, Steven B
APPLICANT: Soreen, Steven B
APPLICANT: Tabaska, Jack B
APPLICANT: Cao, Yongwal
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT APPLICATION DATE: 2003-04-28 US-10-425-114-30672 Sequence 30672, Application US/10425114 ; Publication No. US20040034888A1 ; GENERAL INFORMATION:

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LysArgLysSerGluGluValLeuPheTyrLeuAsnGlyArgCysIleTyrLeuValGly 100
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sequence 9, Application US/10660226
sequence 9, Application US/10660226
sequence 9, Application No. US20040064848A1
GENERAL INFORMATION:
APPLICANT: Cahcon, Rebecca E.
APPLICANT: Famodu, Layo O.
APPLICANT: Hatz, William D.
APPLICANT: History Milliam D.
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SPELOR REPRENCE: BB-1159-C
CURRENT APPLICATION NUMBER: US/10/660,226
CURRENT FILING DATE: 2003-09-11
FRIOR PRIDK APPLICATION NUMBER: US/09/354,501
FRIOR APPLICATION NUMBER: US/09/354,501
FRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER:
SPRIOR FILING DATE: BARLIER FILING DATE: July 21, 1998
NUMBER OF SEQ ID NOS: 28
SOSTINARE: Microsoft Office 97
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 NUMBER OF SEQ ID NOS:
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LENGTH: 1059
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ORGANISM: Zea mays
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Oy 21 ArgHisArgGlyGlyLeuGlnAlaProThrGlySerLeuArgValAlaAspProAlaGly 40 :::	Oy 41 ProAlaValAtaValAtgAlaAtgGlySerLy@ProValAlaProLeuArgLeuArgAla 60	Oy 61 LysLysSerSerGlyGlyHisGluAsnSerHisAsnSerValAspGluAlaLeuLeuLeu 80	Qy 81 LysArgLysSerGluGluValLeuPheTyrLeuAsnGlyArgCysIleTyrLeuValGly 100 	Qy 101 MetMetGlySerGlyLy8SerThrValGlyLy8IleMetSerGluValLeuGlyTyrSer 120 Db 390 ATGATGGGTTCTGGAAAAAGTACTGTGGGGAAGATCTTGTTCTGAAGTCTTATTCG 449	Qy 121 PhePheAspSerAspLysLeuValGluGlnAlaValGlyMetProSerValAlaGlnIle 140	Oy 141 PheLysValHisSerGlualaPhePheArgAspAsnGluSerSerValLeuArgAspLeu 160 	Qy 161 SerSerMetArgArgLeuValValAlaThrGlyGlyGlyGlyAlaValIleArgProIleAsn 180	Oy 181 TrpArgTyrMetLysArgGlyLeuSerValTrpLeuAspValProLeuAspAlaLeuAla 200	Qy 201 ArgArgileAlaLyBValGlyThrAlaSerArgProLeuLeuAspGlnProSerGlyAsp 220	Oy 221 ProfyralaMetalaPheSerLysLeuSerMetLeualaGlnGlnArgGlyAspalafyr 240	Qy 241 AlaAsnAlaAspValArgValSerLeuGluGluIleAlaCysLysGlnGlyHisAspAsp 260	Qy 261 ValSerLysteuThrProThrAspIleAla11eGluSerLeuHislysIleGluSerPhe 280	Oy 281 ValileGluHisThrAlaAspSerSerAlaSerAspAlaGlnAlaGluSerGlnIleGln 300	Qy 301 ArgiledInThrLeu 305 	-35273 273, Application No. US200400348 DRMATION: Liu, Jingdong	; APPLICANT: Zhou, Yihua ; APPLICANT: Kovalic, David K. ; APPLICANT: Screen, Steven E ; APPLICANT: Tabaska, Jack E ; APPLICANT: Cao, Yongwei ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
Qy 141 PhelysValHisSerGluhlaPhePheArgAspAsnGluSerSerValLeuArgAspLeu 160 	Oy 161 SerSerMetArgArgLeuValValAlaThrGlyGlyGlyAlaValIleArgProIleAsn 180 	Oy 181 TrpArgTyrMetLysArgGlyLeuSerValTrpLeuAspValProLeuAspAlaLeuAla 200 	Qy 201 ArgarglleAlaLysValGlyThrAlaSerArgProLeuLeuAspGlnProSerGlyAsp 220 Db 744 AGGGTATTGCTAAAGTGGGAACTGCCTCTCTCTCTCTCTC	Qy 221 ProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnGlnArgGlyAspAlaTyr 240 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	Qy 241 AlaAsnAlaAspValArgValSerLeuGluGluIleAlaCysLysGlnGlyHisAspAsp 260 	Qy 261 ValSerLygLeuThrProThrAspIleAlalleGluSerLeuHisLysIleGluSerPhe 280 	Qy 281 ValileGluHisThrAlaAspSerSerAlaSerAspAlaGlnAlaGluSerGlnIleGln 300 	Qy 301 Arg1leGlnThrLeu 305 Db 1044 AGGATACAGACCTTG 1058	RESULT 3 US-10-425-115-16472 Sequence 16472, Application US/10425115	GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K.	APPLICANT: Cao, Yongwei ; APPLICANT: Cao, Yongwei ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With ; TITLE OF INVENTION: Plants Acid Molecules and Other Molecules Associated With ; TITLE OF INVENTION:	FILE REFERENT APPLICATION NUMBER: US/10/425,115 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 369326	a n		Alignment Scores: 7.59e-159 Length: 1474 Score: 1457.00 Matches: 293 Percent Similarity: 96.72\$ Conservative: 2 Query Match: 95.48\$ Indels: 2 DB: 20 Gaps: 1	US-10-660-226-10 (1-305) x US-10-425-115-16472 (1-1474) Qy

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US-10-42-114-31574

Sequence 31574, Application US/10425114

Sequence 31574, Application US/2014

Publication No. US2004003488A1

APPLICANT: Liu, Jingdong

APPLICANT: Liu, Jingdong

APPLICANT: Zhou, Yihua

APPLICANT: About K.

APPLICANT: About K.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(5313)

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 31574

LENGTH: 1241
                                                                                                81 LysArglysSerGluGluValLeuPheTyrLeuAsnGlyArgCyslleTyrLeuValGly 100
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  GCAAATGCGGATGTAAGGGTTTCTCTGGAAGAGTTGCATCTAAACAAGGTCATGGCGAT 938
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                              ValSerLysLeuThrProThrAspIleAlaIleGluSerLeuHisLysIleGluSerPhe
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Matches:
Conservative:
Mismatches:
Indels:
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US-10-425-114-31574
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Best Local Similarity:
Query Match:
DB:
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Pred. No.:
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    for Plant Improvement
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                                                                                                                                     OTHER INFORMATION: Clone ID: UC-ZMFLTEOSINTE77E09 FLI
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Matches:
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Mismatches:
Indels:
TITLE OF INVENTION: Plants and Uses Thereof
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 35273
LENGTH: 1228
                                                                                             TYPE: DNA
ORGANISM: Zea mays subsp. mexicana
                                                                                                                                                                                         8.09e-151
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121 PhePheAspSerAspLysLeuValGluGlnAlaValGlyMetProSerValAlaGlnIle 140 	141 PhelysvalHisSerGluAlaPhePheArgAspAsnGluSerSerValLeuArgAspLeu 160 	161 SerSerMetArgArgLeuValValAlaThrGlyGlyGlyAlaValIleArgProIleAsn 180 	181 TrpArgTyrMetLysArgGlyLeuSerValTrpLeuAspValProLeuAspAlaLeuAla 200 :::	201 ArgArgilealaLysvalGlyThrAlaSerArgProLeuLeuAspGlnProSerGlyAsp 220 	221 ProTyralaMetAlaPheSerLysLeuSerMetLeualaGlnGlnArgGlyAspAlaTyr 240 	241 AlaAsnAlaAspValArgValSerLeuGluGluIleAlaCysLysGlnGlyHisAspAsp 260 	261 ValSerLysLeuThrProThrAspileAlaileGluSerLeuHisLysIleGluSerPhe 280 	281 ValileGluHisThrAlaAspSerSerAlaSerAspAlaGlnAlaGluSerGlnIleGln 300	301 ArgileGlnThrLeu 305 1055 AGGATACAGACCTTG 1069	115-16474 16474, Application US/10425115	CON TO. USZUG402142/241 TT: La Rosa, Thomas J. TT: Royalic, David K.	NT: Zhou, Yinua NT: Zao, Yongwei F INVENTION: Nucleic Acid Molecules and Other Molecules Associated With F INVENTION: Plants	; FILE REFERENCE: 38-21 153222)B ; CURRENT APPLICATION UNDER: US/10/425,115 ; CURRENT FILING DATE: 2003-04-28 ; NUMBER OF SEQ ID NOS: 369326	Q ID NO 16474 LENGTH: 1583 TYPE: DNA ORGANISM: Zea mays	FEATURE: OTHER INFORMATION: Clone ID: MRT4577_115022C.1 0-425-115-16474	Alignment Scores: Alignment Scores: 1.16e-150 Score: Score: 1387.00 Matches: 278 Percent Similarity: 94.10\$ Best Local Similarity: 91.15\$ Mismatches: 16 Query Match: 20 Gaps: 1 US-10-660-226-10 (1-305) x US-10-425-115-16474 (1-1583)

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Alignment Scores:
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  For Plant Improvement
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279
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                                                                                                 , OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS10471_1
US-10-767-701-13420
                                                                                                                                                                                                           US-10-660-226-10 (1-305) x US-10-767-701-13420 (1-1273)
                                                                                                                                                           Conservative:
Mismatches:
Indels:
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TITLE OF INVENTION: Plants and Uses Thereof FILE REFERENCE: 38-21(5355)B CURRENT APPLICATION NUMBER: US/10/767,701 CURRENT FILING DATE: 2004-01-29 NUMBER OF SEQ ID NOS: 63128 SEQ ID NO L3320
                                                                                                                                        Length:
Matches:
                                                                                                                                       1.14e-146
1351.50
85.67%
83.28%
88.56%
                                                                     TYPE: DNA ORGANISM: Sorghum bicolor
                                                                                                                                                                    Best Local Similarity:
Query Match:
                                                                                                                                                            Percent Similarity:
                                                                                                                              Alignment Scores:
Pred. No.:
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APPLICANT: La ROSAL Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Brazuk, Brad
APPLICANT: Brazuk, Brazuk, Brad
APPLICANT: Brazuk, Brazuk, Brad
APPLICANT: Brazuk, Brazuk, Brad
APPLICANT: Brazuk, Brazuk, Brad
APPLICANT: APPLICANTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NOS: 204966
                                                                                                                                                                                                                                                   947 GAGATTGCATCTAAGCAAGGTCACCATGATGTCTCTAAGCTGACACCCACTGATATCGCA 1006
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CGTCCTCTCCTGGACCAACCATCTGGTGATCCATACACAATGGCCTTCTCTAAGCTCAGC 886
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                                                                      ATGCTTGCAGAGAGAAGGGGTGACGCTTATGCAAATGCAGATGTAAGGGTTTCTCTAGAA
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                                            MetLeuAlaGlnGlnArgGlyAspAlaTyrAlaAsnAlaAspValArgValSerLeuGlu
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Matches:
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Mismatches:
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US-10-437-963-45320
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Publication No. US20040123343A1
GENERAL INFORMATION:
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90.35*
86.17*
85.29*
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ORGANISM: Oryza sativa
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Best Local Similarity:
Query Match:
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RESULT 10
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                ProSerValAlaGlnIlePheLysValHisSerGluAlaPhePheArgAspAsnGluSer
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US-10-660-226-27
Sequence 27, Application US/10660226
Publication No. US20040064848A1
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Fancdu, Layo O.
APPLICANT: Fancdu, Layo O.
APPLICANT: Rendina, Alan
TITLE OF INVENTION: Chorismate Biosynthesis Enzymes
FILE REFERENCE: BB-1159-C
CURRENT APPLICATION NUMBER: US/10/660,226
CURRENT APPLICATION NUMBER: US/09/354,501
PRIOR APPLICATION NUMBER: US/09/354,501
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: G0/093,611
PRIOR PILING DATE: 2003-09-11
PRIOR PILING DATE: EARLIER FILING DATE: July 21, 1998
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 27
LTYPE: NANA
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|CTGACTCACGTGCTCAGAGGATACAGACCTTG 999
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                               Conservative:
Mismatches:
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                                                           Indels:
                                                                      Gaps:
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Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
2.14e-124
1159.00
91.64%
85.45%
75.95%
                             Percent Similarity:
Best Local Similarity:
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Percent Similarity:
Best Local Similarity:
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us-1(
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21 (3322) 8
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
SEQ ID NOS: 369326
SEQ ID NOS: 369326
TYPE: DATA
TYPE: DATA
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US-10-437-963-84942/c
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; Publication No. US20040123343A1
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ORGANISM: Zea mays
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APPLICANT: LA ROSA, Thomas J.
APPLICANT: LA ROSA, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: ADO, Yihua
APPLICANT: Zho, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 84942
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111 sIleMetSerGluValLeuGlyTyrSerPhePheAspSerAspLysLeuValGluGlnAl
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US-10-425-115-68871
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US-10-425-115-68871/c
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                                                --ATGAA
                                                                                                                   glleAlaLysValGlyThrAlaSerArgProLeuLeuAspGlnProSerGlyAspProTy
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US-10-660-226-25

is Sequence 25, Application US/1066026
; Publication No. US20040064848A1
; GENREAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Falco, S. Carl
APPLICANT: Falco, S. Carl
APPLICANT: Rendina Alan
TITLE OF INVENTION: Chorismate Biosynthesis Enzymes
FILE REFERENCE: BB-1159-C
CURRENT FILING DATE: 2003-09-11
PRIOR FILING DATE: 1999-07-16
; PRIOR APPLICATION NUMBER: US/09/354,501
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: SANDER PRIOR FILING DATE: BALLIER APPLICATION NUMBER: SANDER APPLICATION NUMBER: EARLIER APPLICATION NUMBER: SANDER APPLICATION NUMBER: BALLIER APPLICATION NUMBER: SANDER APPLICATION NUMBER: SONDER APPLICATION NUMBER: SANDER APP
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LENGTH: 1323
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Sequence 68871, Application US/10425115

Bublication No. US20040214272A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 68871 432 612 252 Ξ 312 131 151 171 492 493 AGGIGCGCIGATACGACCAATCAATTGGAGTTATATGAAGAAAGGACTCACTATTTG 552 732 : ||| |||| :::|| 133 CCGTGGCGCCAGCCCTGTGCTGCCACAATCGGCAGGTACTGAGAAGCCCA 192 191 211 gProLeuLeuAspGlnProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSerMe 231 251 ulleAlaCysLysGlnGlyHisAspAspValSerLysLeuThrProThrAspIleAlail 271 733 TATTGCATTCAAACAAGGGCATAATGATGTGAATGTACTTACACCAAGTGCCATCGCTAT 792 91

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Falco, S. Carl
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             Length:
Matches:
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56.72%
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Best Local Similarity:
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US-10-660-226-19
      Alignment Scores:
Pred. No.:
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Sequence 19, Application US/10660226 Publication No. US20040064848A1 GENERAL INFORMATION:

APPLICANT: Cahoon, Rebecca E.

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                                                                                                                                     60/093,611
APPLICANT: Famodu, Layo O.
APPLICANT: Hitz, William D.
APPLICANT: Hitz, William D.
APPLICANT: Hitz, William D.
APPLICANT: Hitz, William D.
TITLE GP INVENTION: Chorismate Biosynthesis Enzymes
FILE REFERENCE: B8-1159-C
CURRENT APPLICATION NUMBER: US/10/660,226
CURRENT FILING DATE: 2003-09-11
PRIOR PILING DATE: 1999-07-16
PRIOR APPLICATION NUMBER: BALLIER APPLICATION NUMBER: 60/PRIOR PILING DATE: RABLIER FILING DATE: July 21, 1998
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 19
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CRGANISM: Sorghum
US-10-660-226-19
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                                                                                                                                                                        US-10-660-226-11

US-10-660-226-11

Sequence 11, Application US/10660226

Publication No. US200400648481

GENERAL INFORMATION:
APPLICANT: Falco, S. Carl
APPLICANT: Fancou, Layo O.
APPLICANT: Fancou, Layo O.
APPLICANT: Rendina, Alan
TITLE OF INVENTION: Chorismate Biosynthesis Enzymes
FILE REFERENCE: BB-1159-C
CURRENT APPLICATION NUMBER: US/10/660,226
CURRENT APPLICATION NUMBER: US/09/354,501
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/093,611
PRIOR FILING DATE: BARLIER FILING DATE: J1998
NUMBER OF SEQ ID NOS: 28

SOFTWARE: Microsoft Office 97
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US-10-660-226-11
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Best Local Similarity:
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Pred. No.:
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OM protein

Run on:

Sequence:

Searched:

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Submitted (15-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA

If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB:

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear HTC 16-OCT-2002
             BJ472228
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CB656520
CSJNBC11B
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1 (Sease 1 to 1305)
Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whitsitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Overgo Probes
Unpublished (2002)
2 (bases 1 to 1305)
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AY104682
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CB6
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-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-MODEL=frame+ p2n.model -DEV=xlh
-Q=/Cgn2_1/USFTO_spool/US10660226/runat_25082005_110427_28535/app_query.fasta_1.455
-Q=/Cgn2_1/USFTO_spool/US10660226/runat_25082005_110427_28535/app_query.fasta_1.455
-DB=EST -OPMT=fastap -SUFFTX=ETE -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bite -STRAT=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -TRRANS=000000000
-USFR=pto -NORM=ext -HEAPSIZE=550 -MINLEN=0 -MAXLEN=2000000000
-USFR=US10660226 @CGN 1 1 3437 @runat_25082005_110427_28535 -NCPU=6 -ICPU=3
-NO MAAAP -LARGEQUERS -NEG SCORES=0 -WAIT -DSPEDCCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -TRREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPORT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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CB64025 OSJNEf13C
CB657302 OSJNEc121
CA078453 SCRLAM100
CB656619 OSJNEc11D
BJ248029 BJ248029
CN147205 WOUNDI 48
CB641679 OSJNEDÖIH
CB641679 OSJNEDÖIH
                                                                                                                                                 August 25, 2005, 20:22:28; Search time 3683 Seconds (without alignments) 3152.213 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                   MEAGGVGLALQARAAGFGSS........ADSSASDAQAESQIQRIQTL 305
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                    nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34239544 segs, 19032134700 residues
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Maximum Match 100%
Listing first 45 summaries
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CB657302
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CN147205
CB641679
CB684026
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Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Maximum DB seq length: 2000000000
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1526
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gb_htc:*
gb_est3:*
gb_est6::*
gb_est6::*
gb_gs81:*
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Database

98765

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Result Š. 2

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Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Stregtophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

Ehrhartoideae; Oryzeae; Oryza.

I (bases 1 to 825)

Santasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,

Kudra, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.

Large-scale identification of ESTs involved in the interaction

between rice and Magnaporthe grisea

Unpublished (2003)

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

Renail: http://genome.arizona.edu

Brazi: bray://genome.arizona.edu
                                                         970 GTCTCTAAGGTGATGCCGACTGATATCGCAATTGAGTCACTTCATAAGATCGAGGTTTC 1029
                                                                                                    EST 09-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                +; Site_1: EcoRI; Site_2:
      GCAAATGCGGATGTAAGGGTTTCTCTGGAAGAGATTGCATCTAAACAAGGTCATGGCGAT 969
                                      280
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                                                                                                                                                                                                                                                                     CB684025
OSJNEf13C12.f OSJNEf Oryza sativa (japonica cultivar-group) cDNA

    825
    702anisma="Orryza sativa (japonica cultivar-group)" /mol type="mRNA" /cultivar="Nipponbare"

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Matches:
Conservative:
Mismatches:
Indels:
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/note="Vector: pBluescript II
XhoI; Uninfected Control"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORWARD: gra aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 13 row: C column: 12
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:39947"
/clone="OSJNEf13C12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                         CB684025.1 GI:29687750
                                                                                                                                                                                         1090 AGGATACAGACCTTG 1104
                                                                                                                                                                        301 ArgileGinThrLeu 305
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87.64%
73.89%
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Best Local Similarity:
Query Match:
DB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  611 TTCAAAGTTCACAGTGAAGCCTTCTTTCGGGATAATGAGAGTAGCGTCTTGAGGGATCTG 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SerSerMetArgArgLeuValValAlaThrGlyGlyGlyAlaValIleArgProlleAsn 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TrpArgTyrMetLysArgGlyLeuSerValTrpLeuAspValProLeuAspAlaLeuAla 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             551 TTCTTTGATAGTGACAAATTAGTGGAGCAAGCTGTTGGAATGCCTTCAGTTGCTCAAATA 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ArgargilealalysValGlyThrAlaSerArgProLeuLeuAspGlnProSerGlyAsp 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LysLysSerSerGlyGlyHisGluAsnSerHisAsnSerValAspGluAlaLeuLeuLeu
                                                                                     /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs, this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PheLysValHisSerGluAlaPhePheArgAspAsnGluSerSerValLeuArgAspLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGCGCATTGCTAAAGTGGGAACCGCTTCTCGTCTTTTTGGACCAACCGTCCGGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 ProAlaValAlaValArgAlaArgGlySerLysProValAlaProLeuArgLeuArgAla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 431 AAGAGAAAATCAGAAGAAGTTCTGTTCTACTTAAACGGGGGGGTGTATTTACTTAGTGGGA
/mol_type="mRNA"
/db_xrefe="MaizeDB:636337"
/db_xrefe="taxon:4577"
/clone lib="Maize Mapping Project/DuPont Cornsensus
Library"
                                                                                                                                                                                                                                        1305
275
9
19
3
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Matches:
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1346.00
93.11$
90.16$
88.20$
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COMMENT Contact: Rod Wing Arizona Genomics Institute University of Arizona Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ 85721-0088, USA Tel: 520 621 9288 Email: http://genome.arizona.edu PCR PRIMERS FRIMERS FRANKARD: gga aac agc cgg cca gtg BACKWARD: gga aac agc tat gac cat g Plate: 12 row: I column: 17 Seg primer: gta aaa aga cgg cca gtg. Plate: 12 row: I column: 17 Seg primer: gta aaa aga cgg cca gtg. Iocation/Qualifiers //organism="Oryza sativa (japonica cultivar-group)" //organism="Oryza sativa (japonica cultivar-group)" //db xref="taxon:09947" //lone="OSUNEc12117" //liab_host="makon: 19947" //lab_host="PH108" //lab_host="PH108" //lab_host="DH108" //lab_host="PH108" //lab_host="DH108" //lab_host="Voctor: pBluescript II KS +: Site_1: EcoRI; Site_2: Xho1; 6 hrs after innoculation with Rice Blast (C9240-1)"		MetGluAlaGlyGlyValGlyLeuAlaLeuGlnAlaArgAlaAlaGlyPheGlySer 19	
34 20 35 151 151 75 75 75 325 385	Qy 135 ProSerValAlaGINIIePheLysValHisSerGluAlaPhePheArgAspAsnGluSer 154 CHIRITIAN	Oy 195 ProLeuAspAlaLeuAlaArgArg1leAlaLysValGlyThrAlaSerArgProLeuLeu 214 [SULT 3 SULT 3 SULT 3 SULT 3 CUS CUS CUS CUS CUS CUS CUS CUS CONDEC1217.f OSUNEC ORY CLORO OSUNEC1217.f OSUNEC ORY CLORO OSUNEC1217.f OSUNEC ORY CLORO CONTROL OSUNEC ORY CRESTON CREST

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Triticum aestivum (bread wheat)

Ish Triticum aestivum

Ebkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Ebkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooldeae; Triticaee; Triticum.

SS Ogihara; V. and Murai, K.

Expressed genes in Triticum aestivum

L Unpublished (2002)

Contact: Tadasu Shin-i

Center For Genetic Resource Information

National Institute of Genetics

Illl Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6856

Fax: Location/Qualifiers

Location/Qualifiers
                                                                                                                                                                                                                                                                                                    BJ248029 C. Ogihara unpublished cDNA library, Wh_f Triticum aestivum cDNA clone whf4j22 5', mRNA sequence.
BJ248029.1 GI:20059002
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          /mol_type="mRNA"
/cultivar="Chinese Spring"
/cultivar="Chinese Spring"
/db xref="taxon:4565"
/clone="whf4j22"
/tissue type="spike at flowering date"
/dev stage="Feekes' scale 10.5.1"
/clone_lib="Y. Ogihara unpublished cDNA library,
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/organism="Triticum aestivum"
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Tel: 520 626 3967

Fax: 520 621 9288

Email: http://genome.arizona.edu
PCR PRimers
PCR PRimers
FORWARD: gqa aaa cga cgg cca gtg
BACKWARD: gqa aaa cga cgg cca gtg
Location/Qualifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Sorghum.

(bases 1 to 804)

Cordonnier-Pratt, M.-M., Suzuki, Y., Sugano, S., Klein, R.R., Liang, C., Sun, F., Sullivan, R., Brady, J., Eastman, A., Miller, V., Gonzalez, M., Anfuso, C., Chhabra, D., Johnson, H., Kamran, D. and Pratt, L.H.

A Sorghum EST database: mechanically damaged and methyl

Jasmonate-treated leaves

Unpublished (2003)

Cother ESTS: WOUND1 48 G03.g1 A002

Contact: Cordonnier-Pratt MM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mmpratt@dga.edu
Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
the Human Genome Center, University of Tokyo Institute of Medical
Science: plant material and RNA prepared at Texas A & M University,
sequencing done in the Laboratory for Genomics and Bioinformatics,
University of Georgia. Sequence ends have been trimmed to exclude
vector and regions below Phred quality 16. Three-prime sequences
are presented as their reverse complement and have been trimmed to
exclude polyA.
Seq primer: Sug3-14 (TAGTCTAGCGGCGCGACC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CN147205 804 bp mRNA linear EST 01-APR-2004 WOUND1 48 G03.bl A002 Wounded leaves Sorghum bicolor cDNA clone WOUND1-48-G03_A002_3', mRNA sequence.

CN147205_1 GI:45987613
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241 AlaAsnAlaAspValArgValSerLeuGluGluIleAlaCysLysGlnGlyHisAspAsp
                                                                                                                                    TCCTCAATGCGGGGATTAGTTGTTGCTACTGGAGGTGGTGCTGTTATCCGACCTGTTAAC
                                                                                                                                                                                              ArgArgIleAlaLysValGlyThrAlaSerArgProLeuLeuAspGlnProSerGlyAsp
                                                                                                                                                                                                                                                          AGGCGTATTGCTAAAGTGGGGAGACTGCCTCGCGTCTTCTAGATCAACCATCCGGCGAT
                                                                                                                                                                                                                                                                                                   ProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnGlnArgGlyAspAlaTyr
                                                                                                                                                                                                                                                                                                                      295 TICAAGGIICACAGIGAAGCCIICTICAGGGAIAAIGAGAGIAGIGICTIGAGGGAITIG
                                                                                                                   SerSerMetArgArgLeuValValAlaThrGlyGlyGlyAlaValIleArgProlleAsn
                                                                                                                                                                                TrpArgTyrMetLysArgGlyLeuSerValTrpLeuAspValProLeuAspAlaLeuAla
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 583 0210
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                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCTCTAAGCTGACGCCGATTGATATTGCTCTG 687
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CN147205
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Location/Qualifiers

FEATURES

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/db xref="taxon:4558"
/dlone=woundl 48 G03 A002"
/dlone=woundl 48 G03 A002"
/dlone lib="wounded leaves"
/dlone lip library was prepared from polyA+ RNA
harvested from 8-day-old hydroponically grown, BTx623
harvested from 8-day-old hydroponically grown, BTx623
leaf ws crushed without damaging the midvein. For others,
methyl jasmonate was added to the growth medium to a final
concentration of 100 uM. Leaves were harvested 3 and 27 hr
after treatment and pooled. Double-stranded cDNA was
cloned unidirectionally into different brailI sites of the
pwhiles-FIJ vector (5-prime DrailI site is CACTGTGTG,
3-prime DrailI site is CACCATGTG). Xhol excises the CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AlaValGlyMetProSerValAlaGlnIlePheLysValHisSerGluAlaPhePheArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MetLeualaGlnGlnArgGlyAspAlaTyrAlaAsnAlaAspValArgValSerLeuGlu
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201
7
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0
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Matches:
Conservative:
Mismatches:
Indels:
organism="Sorghum bicolor"
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                    mol_type="mRNA"
cultivar="BTx623"
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1013.00
96.74%
93.49%
66.38%
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Best Local Similarity:
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CB684026

S18 bp mRNA linear EST 09-APR-2003
OSJNEf13C12.r OSJNEf Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEf13C12 3', mRNA sequence.
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Oryza sativa (japonica cultivar-group)
Cukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Enthartoideae; Oryzae; Oryza.

I (bases 1 to 81)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          546
                                                                                                                                                                                                                                                                                                                                                                                                       135 ProSerValAlaGlnIlePheLysValHisSerGluAlaPhePheArgAspAsnGluSer 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerValLeuArgAspLeuSerSerMetArgArgLeuValValAlaThrGlyGlyGlyAla 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  547 AGIGICTIGAGGAITIGICCTCAAIGAAGCGAITAGITGITGCTACIGGAGGIGGIGCI 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VallleArgFrolleAsnTrpArgTyrMetLysArgGlyLeuSerValTrpLeuAspVal 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  667 CCCTTGGACGCTCTTGCTAGGCGTATTGCTAAAGTGGGGACTGCCTCCCGTCCTTCTA 726
366
                                                                                                                                                                                       95 CysileTyrLeuValGlyMetMetGlySerGlyLysSerThrValGlyLysIleMetSer 114
                                                                                                                                                                                                                           367 IGHTHITTACCTAGTTGGAATGATGGGTTCTGGAAAAAGTACTGTGGGAAAGGATCATGTCT 426
                                                                                                                                                                                                                                                                                                  GluValLeuGlyTyrSerPhePheAspSerAspLysLeuValGluGlnAlaValGlyMet 134
                                                                                                                                                                                                                                                                                                                                    GAAGTTTTGGGTTATTCGTTCTTTGATAGTGATAAATTGGTCGAACAAGCTGTGGGCATG 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AspGlnProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGln 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                727 GATCAACCATCTGGTGATCCATACACAATGGCTTTTTTCTANACTCAGCATGCTCGCGGGG 786
                                                                                                           307 GATGAAGCCTCTTGCTAAAGAGAAAATCAGAAGAAGAGTTCTCTTCTATTTGAATGGACGG
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                                                                              75 AspGluAlaLeuLeuLysArgLysSerGluGluValLeuPheTyrLeuAsnGlyArg
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                                                                                                                                                                                                                                                          Oryza sativa (japonica cultivar-group)

Gryza sativa (japonica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.

I (basea 1 to, 79)

Skudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.

Large-Grale identification of ESTs involved in the interaction between rice and Magnaporthe grisea

Unpublished (2003)

Contact: Rod Wing

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Fax: 520 625 3967

Fax: 520 625 3967
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/organism="Oryza sativa (japonica cultivar-group)"
/organism="Oryza sativa (japonica cultivar-group)"
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/clone_lib="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2: Xhof; 24 hrs after innoculation with Rice Blast (Che 86061)"
                                                                                                        CB641679 1797 bp mRNA linear EST 08-APR-2003 OSJNEb01H04.f OSJNEb Oryza sativa (japonica cultivar-group) cDNA clone OSJNEb01H04 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 SerArgHisArgGlyGlyLeu------GlnAlaProThrGlySerLeuArg 34
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  AGCGACTCGCAAGCTGAGTCGCAGATCCAAAGGATACAGACCTTG 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 797
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Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 01 row: H column: 04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: http://genome.arizona.edu
PCR PRimers
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/db_xref="rexponents"
/clone="MSJNBc11B01"
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                  EST.

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Oryza sativa (idiponica cultivar-group)

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaae; Oryza.

1 (Jasses 1 to 772)

Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,

Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.

Large-scale identification of ESTs involved in the interaction

Unpublished (2003)
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/mol type="mRNA"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                           ΑZ
                                                                                                                                                                                                                                Contacts: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson,
85721-0088, USA
Pex: 520 626 3967
Fex: 520 621 9288
Email: http://genome.arizona.edu
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Matches:
Conservative:
Mismatches:
Indels:
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BACKWARD: gga aac agc tat gac cat g
Plate: 11 row: B column: 01
Seq primer: gta aaa aga cgg cca gtg.
Location/Qualifiers
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       GI:29660283
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86.97%
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/lab_host="PH10B"
/clone lib="0SANRE"
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OSJNEC11B01.f OSJNEC Oryza sativa (japonica cultivar-group) CDNA
Clone OSJNEC11B01 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LeuAlaGlnGlnArgGlyAspAlaTyrAlaAsnAlaAspValArgValSerLeuGluGlu 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 IlealaCysLysGlnGlyHisAspAspValSerLysLeuThrProThrAspIleAlaIle 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GluSerLeutisLysIleGluSerPheValIleGlutisThrAlaAspSerSerAlaSer 291
                                                                                                                                                                                                                                                                                                                                                                                                                                        AATGGACGGTGTATTTACCTAGTTGGAATGGTTCTGGAAAAAGAAAAGTACTGTGGGAAAG
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Conservative:
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640 bp mRNA linear EST 23-MAY-2002 BJ47228 K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA BJ472228 BJ472228.1 GI:21150731
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Hordeum vulgare subsp. vulgare
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
I (bases 1 to 640)
Sato, K., Saisho, D. and Takeda, K.
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2002)
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Mismatches:
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                                                                                                                                          Gaps:
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                   5.38e-91
972.00
95.71%
90.95%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (japonica cultivar-group)

ENKaryora, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;

Eukaryora, Viridiplantes, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryzeae; Oryzeae;

Enthartoideae; Oryzeae; Oryzeae; Oryzeae;

Santasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E., Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.

Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea

Unpublished (2003)

Contact: Rod Wing

Arizona Genomics Institute
University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

Fax: 520 621 9288

Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: gga acc agc tat gac cat g.

Location/Qualifiers

1. 854

| Location="Oryza sativa" (japonica cultivar-group)" |
| mol type="mmkNa" |
| clone="Osymbolare" |
| db xref="taxon:39947" |
| clone="Osymbol2117" |
| tissue_type="leaf" |
| dev stage="3 week" |
| lab_host="DH108" |
| clone="lib="OSJNBc" |
| clone="lib="OSJNBc" |
| note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2: NhoI; 6 hrs after innoculation with Rice Blast (C9240-1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST 09-APR-2003
                                                                                                                                                                                                                                 SerValLeuArgAspLeuSerSerMetArgArgLeuValValAlaThrGlyGlyGlyGlyAla 174
                                                                                                                                                                                                                                                                                                                             ValileArgProileAsnTrpArgTyrMetLysArgGlyLeuSerValTrpLeuAspVal 194
                                                                                                                                                                                                                                                                                                                                                                                                                        ProLeuAspAlaLeuAlaArgArg1leAlaLysValGlyThrAlaSerArgProLeuLeu 214
                                               134
                                                                                                                                          154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             954 bp mRNA linear EST 09-APR-20 OSJNEC12117.r OSJNEC Oryza sativa (japonica cultivar-group) cDNA clone OSJNEC12117 3', mRNA sequence. CE657303 CE657303.1 GI:29661028
                                          TGTATTTACCTAGTTGGAATGATGGGTTCTGGAAAAAGTACTGTGGGGAAAGATCATGTCT
                                                                                                                                   FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 12 row: I column: 17
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195

554

135 734 674

215

494

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// Mol type="mana" | Mol type="mana" | Mol type="mana" | Mol xref="taxon.4547" |
| Ab xref="taxon.4547" |
| Ab host="bythor" | Ab the type | Mol type | Mo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complex.

1 (bases 1 to 672)

S. Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda P
Contract: Arruda P
Contract Arruda P
Contro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Universidade Estadual de Campinas
Sira Postral 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1137
F
                                                                                                           6/2 bp mRNA linear EST 24-SEP-2003
SCVPRT2077E07.g RT2 Saccharum officinarum cDNA clone SCVPRT2077E07
5', mRNA sequence.
CA146167
                                                                                                                                                                                                                                                                                                                                                                                                                        Saccharum officinarum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MetGlualaGlyGlyValGlyLeualaLeuGlnalaArgAlaAlaGlyPheGlySerSer
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/organism="Saccharum officinarum"
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TITLE
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SerValAlaGlnIlePheLysValHisSerGluAlaPhePheArgAspAsnGluSerSer 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValLeuArgAspLeuSerNetArgArgLeuValValAlaThrGlyGlyGlyAlaVal 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 TTGGAAGCTCTTGCAAGGCGTATTGCTAAAGTGGGGACTGCCTCGCGTCCTCTTCTAGAT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   542
                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mkNa" //mol_type="mkNa" //mol_type="mkNa" //mol_type="mkNa" //mol_type="mkNa" //mol_type="mkNa" //mol_type="kop three leaves" //mol_type="kop thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 GTCTTGAGGGATTTGTCCTCTATGCGGCGATTAGTTGTTGCTACTGGAGGTGGTGCTGTT 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 GlnProSerGlyAspProTyrAlaMetAlaPheSerLysLeuSerMetLeuAlaGlnGln 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ArgGlyAspAlaTyrAlaAsnAlaAspValArgValSerLeuGluGluIleAlaCysLys 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    76 GluAlaLeuLeuLeuLysArgLysSerGluGluValLeuPheTyrLeuAsnGlyArgCys 95
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                                                                                                                                                                                                                                                                                                                                      subsp. vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               640
191
7
0
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
TE1: 81-559-81-6856
Fax: 81-559-81-6855
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                          Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
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968.00
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OSJNEC11B01.r OSJNEC Oryza sativa (japonica cultivar-group) cDNA clone OSJNEc11B01 3', mRNA sequence. CE656559 GI:29660284
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaae; Oryza.
1 (bases I to 789)
Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E., Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
prepared by mass excision."
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97.51%
95.02%
62.91%
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Organism="Sorghum bicolor"
/mol_type="mRNA"
/db xref="taxon:4558"
/clone_lib="Light Grown (LG1)"
/note="Organ: 10- to 14-day-old light-grown (greenhouse)
seedlings; Vector: Lambda Zap; Site 1: XhoI; Site 2:
ECORI; The library was made from poly-A RNA in the cloning
vector lambda ZAP II. Clones to be sequenced were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW671996

609 bp mRNA linear EST 19-JUL-2000
LG1_353_A11.b1_A002 Light Grown 1 (LG1) Sorghum bicolor cDNA, mRNA
sequence.
AW671996.1 GI:7535901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Cordonier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
                                                                  100
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Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 609)

Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C. and Pratt, L. H.

An EST database from Sorghum: light-grown seedlings
              80
           MetMetGlySerGlyLyBSerThrValGlyLySileMetSerGluValLeuGlyTyrSer
                                                                                                                                  PhePheAspSerAspLysLeuValGluGlnAlaValGlyMetProSerValAlaGlnIle
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High quality sequence stop: 607
POLYA=No.
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279 SerPheVallleGluHisThrAlaAspSerSerAlaSerAspAlaGlnAlaGluSerGln 298
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Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea

Unpublished (2003)

Contact: Rod Wing

Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 624 3967
Fax: 520 624 3967

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                            OM protein - protein search, using sw model
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August 25, 2005, 10:33:33 ; Search time 64 Seconds (without alignments) 2440.377 Million cell updates/sec US-10-660-226-10 1526 1 MEAGGVGLALQARAAGFGSS.....ADSSASDAQAESQIQRIQTL 305 Title: Perfect score: Sequence: Run on:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1612378 segs, 512079187 residues Searched:

1612378 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	de			SUMMARIES	
Score		Query Match Length DB	DB	ID	Description
852	55.8	287	6	Q7X7H9	O7x7h9 oryza gativ
655		303	~	Q8GT76	arabid
649.5		292	н	AROK ARATH	
642.5	4.	300	٦	AROK_LYCES	
606.5		300	~	Q8GY88	
440	N	157	~	Q6PLR3	
429	~	305	~	Q9SVA4	_
340.5	N	190	~	Q7VE85	
338.5	22.2	177	~	Q7NH27	Q7nh27 gloeobacter
338.5	, 22.2	181	~	Q8YXG9	Q8yxg9 anabaena sp
331.5			N	Q9LW20	
318.5			٦	AROK SYNY3	P72796 synechocyst
312.5		191	~	Q7U469	
:	20.4		٦	AROK SYNEL	Q8dkh7 synechococc
283		192	N	Q7V9 <u>0</u> 4	
272.5			~	Q7V3G8	Q7v3g8 prochloroco
267.5		244	7	Q89XW7	Q89xw7 bradyrhizob
262		175	0	Q74BL5	•
256.5			7	Q6NCG8	
254.5	7	210	~	Q6G1N9	
250	٦	210	7	0661н5	O6g1h5 bartonella
249.5	_	168	-	AROK AQUAE	067925 aquifex aeo
246	16.1	265	0	Q655 <u>K</u> 8	
242.5	15.9	174	7	Q67N09	
239.5	_	171	7	QBRAE8	Q8rae8 thermoanaer
237.5	_		-	ARKB THEMA	Q9wyi3 thermotoga
235	-	180	7	Q6F7E4	O6f7e4 acinetobact
235	15.4	211	~	Q82TC0	082tc0 nitrosomona
234.5	7	200	~	Q9A435	Q9a435 caulobacter
228.5	_	184	~	Q7NZU3	
227	7	186	7	Q7MUD6	Q7mud6 porphyromon

ALIGNMENTS

	4.	59	119
PRELIMINARY; PRT; 287 AA. 07X719 07X719 07X719; 07X602; 07X602. 01-COT-L2003 (TERMELTel. 25, Last sequence update) 01-COT-2003 (TERMELTel. 25, Last sequence update) 01-COT-2003 (TERMELTel. 25, Last sequence update) 02-UUL-2004 (TERMELTel. 27, Last annotation update) 02SUNBBO079B02.2 protein (OSYMBBD003B01.21) Name=OSYMBBO079B02.2; SYNDAMS-SCANBBD003B01.21; Name=OSYNBBO079B02.2; SYNDAMS-SCANBBD003B01.21; DAYZa sativa (japonata cultivar-group) Name=OSYNBBO079B02.2; SYNDAMS-STEPPOPHYLS; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Shermatodeae; Oryzees; Oryza. NCBI TaxiD=39947; NCBI TaxiD=39949; NCBI T	55.8%; Score 852; DB 2; Length 287; Similarity 64.1%; Pred. No. 2.4e-57; 2; Conservative 37; Mismatches 61; Indels 4; Gaps	1 MEAGGVGLALQARA-AGFGSSRHRGGLQAPTGSLRVADPAGPAVAVRARGSKPVAPLRLR 59	60 AKKSSGGHENSHNSVDEALLLKRKSEEVLFYLNGRCIYLVGMMGSGKSTVGKIMSEVLGY 119 ::: 58 CSRKPAGIDKTYYSADEALVLKQKAEDVVPYLNDRCIYLVGMMGSGKTTVGKILAEVLGY 117
RESULT 1 07X7H9 ALC 07X7H9 DD 07X7H9 DD 07X7H9 DD 01-OCT DD 05-JUL- DD 05-J	Query Match Best Local Matches 18		
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NWRYMKRGLSVWLDVPLDALARRIAKVGTASRPLLDQPSGDPYAMAFSKLSMLAQQRGDA 239
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SFFDSDKLVEQAVGMPSVAQIFKVHSEAFFRDNESSVLRDLSSMRRLVVATGGGAVIRPI
                      118 SFFDSDKLVEKAVGISSVAEIFQLHSEAFFRDNESEVLRDLSSMHRLVVATGGGAVIRPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantee, Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,
Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,
Hayashizaki Y., Shinozaki K.;
Submitted (NOV-2005) to the EMBL/GenBank/DDBJ databases.
EMBL, AK118899; BAC43483.2; --
HSSP; P10880; 1SHK.
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                                                                                                                                                                     240 YANADVRVSLEEIACKOGHDDVSKLTPTDIAIESLHKIESFVIE
                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004765; F:Bhikimate kinase activity; IEG
GO; GO:0008652; P:Bhikimate kinase.
TEA-INTERPROFESS; P:BHIKIMATE BEA-INTERPROFESS; IEA-INTERPROFESS; SKI; I.
PFam; PF01202; SKI; I.
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(Rel. 41, Last sequence update)
(Rel. 44, Last annotation update)
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+ive 36; Mismatches
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PROSITE; PS01128; SHIKIMATE_KINASE; 1.
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                                                                                                                                                                                                                                                                                                                                                              Created)
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les 127; Conservative
                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=At2g21940;
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Q9SJ05;
28-FEB-2003
28-FEB-2003
05-JUL-2004
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        139 QIFKVHSEAFFRDNESSVLRDLSSMRRLVVATGGGAVIRPINWRYMKRGLSVWLDVPLDA 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88 ILKRKAREVKPYLNGRSMYLVGMMGSGKTTVGKLMSKVLGYTFFPCDTLIEQAMNGTSVA
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                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=cv. Columbia;
MEDINIB=20083487; PubMed=10617197; DOI=10.1038/45471;
MEDINIB=20083487; PubMed=10617197; DOI=10.1038/45471;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D., Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V., Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L., Moffat K.S., Cronin L.A., Shen M., Pai G., Van Aken S., Umayam L., Tallon L.J., Gill J.B., Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                        eudicots; rosids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P10880; 1SHK.
InterPro; IPR000623; Shik_kinase.
Pfam; PF01202; SKI; SKIKINTKNASE.
PRINTS; PR01100; SHIKINTKNASE.
PROSITE; PS01128; SHIKIMATE_KINASE; 1.
Aromatic amino acid biosynthesis; ATP-binding; Chloroplast; Kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 402:761-768(1999).
-!- CATALYTIC ACTIVITY: ATP + shikimate = ADP + shikimate 3-phosph
-!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fifth step.
-!- SUBCELLULAR LOCATION: Chloroplast (By similarity).
-!- SIMILARITY: Belongs to the shikimate kinase family.
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Probable shikimate kinase.
ATP (By similarity).
42C9DE79D7EE54B7 CRC64;
OrderedLocusNames=At2g21940; ORFNames=F7D8.26;
Arabidopsis thaliana (Mouse-ear cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicoryledons; core eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Best Local Similarity
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01-MAR-2003 (TrEMBLrel. 23, Created)
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                                                                                                                                                                                                                                 NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   133 GMPSVAQIFKVHSEAFFRDNESSVLRDLSSMRRLVVATGGGAVIRPINWRYMKRGLSVWL 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVPLDALARRIAKVGTASRPLLDQPSGDPYAMAFSKLSMLAQQRGDAYANADVRVSLEEI 252
                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids, lamiids, Solanales, Solanaceae, Solanum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- CATALYTIC ACTIVITY: ATP + shikimate = ADP + shikimate 3-phosphate. -!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
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HSSP; P10880; 1SHK.
INTERPO, 1EPR0006523; Shik_kinase.
PFam; PF01202; SKI; 1.
PRINTS; PR01100; SHIKIMTKNASE.
PROSITE; PS01128; SHIKIMATE KINASE; 1.
Aromatic amino acid biosynthesis; ATP-binding; Chloroplast; Kinase;
                                                                                                                                                                                                                                                                                                                           STRAIN=cv. UC82B; TISSUE=Leaf;
MEDLINE=32727054; PubMed=1338949;
Schmid J., Schaller A., Leibinger U., Boll W., Amrhein N.;
Schmid J., Schaller A., Leibinger U., Boll W., Amrhein N.;
"The in-vitro synthesized tomato shikimate kinase precursor is arrymatically active and is imported and processed to the mature enzyme by chloroplasts";
Plant J. 2:375-383(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 42.1%; Score 642.5; DB 1; Length Best Local Similarity 60.3%; Pred. No. 3.2e-41; Matches 126; Conservative 35; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fifth step.
-!- SUBCELLULAR LOCATION: Chloroplast.
-!- SIMILARITY: Belongs to the shikimate kinase family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chloroplast (Potential).
Shikimate kinase.
ATP (By similarity).
, 9CDAC8136922CCB3 CRC64;
                                             01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Shikimate kinase, chloroplast precursor (EC 2.7.1.71)
Lycopersicon esculentum (Tomato).
  300 AA
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STANDARD;
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         NCBI_TaxID=4081;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  193
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Q8GY88
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300 AA

PRELIMINARY;

Q8GY88 Q8GY88;

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115 GKIMARSLGYTFFDCDTLIEQAMKGTSVAEIFEHFGESVFREKETEALKKLSLMYHQVVV 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      169 ATGGGAVIRPINWRYMKRGLSVWLDVPLDALARRIAKVGTASRPLL-DQPSGDPYAMAFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 RLRA---KKSSGGHENS---HNSVD-EALLLKRKSEEVLFYLNGRCIYLVGMMGSGKSTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                       Name=At4g39540/P23K16 170;
Arabidopais thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                      [2]
SEQUENCE FROM N.A.
Chan H., Cheuk R., Shinn P., Bowser L., Carninci P.,
Chan M., Chang C.H., Dale J.M., Hayashizaki Y., Hauan V.W.,
Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,
Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Onodera C.S.,
Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
Shinnozaki K., Davis R.W., Theologis A., Ecker J.R.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AK117791; BAC42436.1;
EMBL, ENDAZS1, AAC63355.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shikimate kinase (Fragment).
Cucumis sativus (Cucumber).
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
                                                                                                                                                                                                                                                                                                                                J.,
Kawai J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228 KLSMLAQQRGDAYANADVRVSLEEIACKQGHDDVSKLTPTDIAIESLHKIESFV 281
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; Pred. No. 1.9e-38;
37; Mismatches 58; Indels 9.
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida
Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P.,
Hayashizaki Y., Shinozaki K.;
Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       300 AA; 33777 MW; 8868B7DF6FF7D492 CRC64;
01-MAR-2003 (TrEMBLrel. 23, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Putative shikimate kinase (At4939540).
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005524, F:ATP binding; IEA.
GO; GO:0004765; F:Bhikimate kinase activity; IEA.
GO; GO:0008652; P:amino acid biosynthesis; IEA.
InterPro; IPR000680; Shik_kinase.
InterPro; IPR001680; WD40.
PRINTS; PR01100; SHIKIMTKNASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01128; SHIKIMATE KINASE; UNKNOWN_1.
PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 AA
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55.6%;
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PROSITE; PS00678; WD_REPEATS_1; UNKNOWN_1.
                                                                                                                                      88;
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                                           SEQUENCE
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                                                                                         Query Match
                          Kinase.
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                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 SVAEVFKVYGEDFFRERETEALRKLSLARQFVISTGGGAVTRSINWKYMHKGISVWLDVP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murphy G., Ridley P., Hudson S., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, ALO78620; CAB44689.1; --
EMBL, ALI61595; CAB80617.1; --
PIR; T09370; T09370.
HSSP; P10880; 1SHK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name-AT4939540;
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                    28.8%; Score 440; DB 2; Length 157; 58.2%; Pred. No. 5.4e-26; ive 27; Mismatches 34; Indels
                                                            Kim M.S., Yang K.Y., Kim Y.C., Cho B.H.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AYS96190; AAT02351.1; -.
HSSP; P24167; 1KAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                       157 AA; 17514 MW; 378B1883D8F9E7F2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Shikimate kinase-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mostrical Colonoscial Figure 1 Part Principal Colonoscial Figure 1 Part Principal Colonoscial Figure 1 Part Principal Colonoscial Premino acid biosynthesis; IEA. Interpro; IPR001623; Shik kinase. Interpro; IPR001680; WD40. PRINTS; PR01100; SHIKIMTKNASE. PR051128; SHIKIMATE_KINASE; UNKNOWN_1.
                                                                                                                                                       GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004765; F:8hikimate kinase activity; IE
GO; GO:0004652; P:amino acid biosynthesis; IEA.
InterPro; IPR000623; Shik kinase.
Pfam; PF01202; SKI; 1.
PRINTS; PR01100; SHIKIMTKNASE.
PROSITE; PS01128; SHIKIMATE_KINASE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256 QGHDDVSKLTPTDIAIESLHKIESFV 281
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01-MAY-2000 (TrEMBLrel. 13, Last seq
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Best Local Similarity
Matches 85; Conserv
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                                             SEOUENCE FROM N.A.
  NCBI_TaxID=3659;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 RRIAKVGTASRPLLDQPSGDPYAMAFSKLSMLAQQRGDAYANADVRVSLEEIACKQGHDD 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=SARG / CCMP 1375 / SS120;
STRAIN=SARG / CCMP 1375 / SS120;
STRAIN=SARG / CCMP 1375 / SS120;
STRAIN=Z2810154; PubMed=12917466; DOI=10.1073/pnas.1733211100;
Dufreene A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M., Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F., Makarova K.S., Ostrowski M., Oztas S., Robert C., Rogozin I.B., Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P., "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120, a nearly minimal oxyphototrophic genome.";
Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).
HSSP: P24167; IKAG.
                                                                                                                                                                                                                                                                        PINWRYMKRGLSVWLDVPLDALARRIAKVGTASRPLL-DQPSGDPYAMAFSKLSMLAQOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 KRKSEEVLFYLNGRCIYLVGMMGSGKSTVGKIMSEVLGYSFFDSDKLVEQAVGMPSVAQI
                                                                                                                                                            119 YSFFDSDKLVEQAVGMPSVAQIFKVHSEAFFRDNESSVLRDLSSM-RRLVVATGGGAVIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                Length 305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae; Prochlorococcus.
                                                                                                                                                                                                                                                                                                                                                                                    GDAYANADVRVSLEEIACKQGHDDVSKLTPTDIAIESLHKIESFV 281
                                                                                                                                                                                                                                                                                                                                                                                                                    249 GEAYTKASARVSLENITLKLGYRSVSDLTPAEIAIEAFEQVQSYL 293
                                                                                                      47; Indels
305 AA; 34744 MW; 9C08637565FE59FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21555 MW; 827831CEB8C141AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004765; F:Bhikimate kinase activity; IEA.
GO; GO:0008652; P:amino acid biosynthesis; IEA.
InterPro; IPR000623; Shik kinase.
PROSITE; PS01128; SHIKIMATE_KINASE; 1.
                                                   28.1%; Score 429; DB 2; 53.3%; Pred. No. 8.5e-25; tive 28; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190 AA
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Name=arok; OrderedLocusNames=Pro0128;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome; Kinase. SEQUENCE 190 AA; 21555
                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prochlorococcus marinus.
                                                                               Local Similarity
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MEDLINE=21595285; PubMed=11759840;
                                                                                                                                                                                                      Query Match
Best Local Similarity 40.5*
Matches 81; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clones.";
                                                                                                                                                                                                                                                                                                                                            211
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                                                                                                                     HSSP;
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Q9LW20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRPLLDQPSGDPYAMAFSKLSMLAQQRGDAYANADVRVSLEEIACKQGHDDVSKLTPTDI 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ----PPAV 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T., Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Takeuchi C., Yamada M., Tabata S., Tokeuchi C., Yamada M., Tabata S., "Complete genome structure of Gloeobacter violaceus PCC 7421, a cyanobacterium that lacks thylakoids."; BMBL, AP006577; BAC90651.1; -. HSSP: P24167; IKAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                      Length 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OrderedLocusNames=alr1244;
Anabaena sp. (strain PCC 7120).
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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SEQUENCE 177 AA; 19103 MW; 37C8E120E5E6F018 CRC64;
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                                                                                                                                          Gloeobacter violaceus.
Bacteria; Cyanobacteria; Chroococcales; Gloeobacter.
NCBI_TaxID=33072;
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Last annotation update)
                                                                                                            Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                           61;
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GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004765; F:Shikimate kinase activity; IEA.
GO; GO:0006652; F:Shikimate kinase activity; IEA.
INCEPEO; IPRO00623; Shik kinase.
PRINTS; PRO1100; SHIKIMTKNASE.
PROSITE; PS01128; SHIKIMATE KINASE; 1.
                                                                                                 sequence update)
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43.1%; Pred. No. 3.9e-18;
iive 28; Mismatches 61
                                                                 177 AA
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                                                                                                                                Name=aroK; OrderedLocusNames=glr2710;
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--RETPEEVALVIFKKLSEII 185
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STRAIN=PCC 7421;
MEDLINE=22977040; PubMed=14621292;
                                                                                                  Last
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160 AEETLRCLAARLAEDSA 176
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                                                                                     01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26,
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tes 85; Conservative
                                                                 PRELIMINARY;
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NCBI_TaxID=103690;
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                                                                                                                      Shikimate kinase
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151 DNESSVLRDLSSMRRLVVATGGGAVIRPINWRYMKRGLSVWLDVPLDALARRIAKVGTAS 210
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"Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
features of the regions of 4,504,864 bp covered by sixty Pl and TAC
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2004 (TrEMBLrel. 15, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
15-JUL-2004 (TrEMBLrel. 27, Last annotation)
16-JUL-2004 (TrEMBLRel. 27, Last a
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Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S., Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120.";
EMBL; AP003585; BAB73201.1; -.
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SEQUENCE FROM N.A.
Shinn P., Chen H., Cheuk R., Kim C.J., Ecker J.R.;
Shinn P., Chen H., Cheuk R., Kim C.J., Ecker J.R.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
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Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
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GO; GO:0004765; F:Shikimate kinase activity; IEA.
GO; GO:0008652; F:Shikimate kinase activity; IEA.
GO; GO:0008652; F:Shikimate kinase activity; IEA.
COMPLETE PROLIOO; SHIKIMTKNASE.
COMPLETE PROLEOME; KINASE.
SEQUENCE 181 AA; 19816 MW; ZE89FBAC8D32FE03 CRC64;
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MEDLINE=20277480; PubMed=10819329;
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                                                                                                                                                                                                                                              53 VAPLRLRAKKSSGGHENSHNSVDEALLLKRKSEEVLFYLNGRCIYLVGMMGSGKSTVGKI 112
                                                                                                                                                                                                                                                                169 GAVQSLRNLALLRHGISIWIDVPLDITAKG------DDDSFHSEPSPELFDTLK 216
                                                                                                                                                                                                                                                                                                      113 MSEVLGYSFFDSDKLVEQAVGMPSVAQIFKVHSEAFFRDNESSVLRDLSSMRRLVVATGG 172
                                                                                                                                                                                                                                                                                                                                                              173 GAVIRPINWRYMKRGLSVWLDVPLDALARRIAKVGTASRPLLDQPS--GDPYAMAFSKLS 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y., Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Mateuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- CATALYTIC ACTIVITY: ATP + shikimate = ADP + shikimate 3-phosphate.
-i- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence analysis of the genome of the unicellular cyanobacterium Symechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-1136(1996).
                                                                                                                                                                                                                   15;
                                                                                                                                                                                      Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                       231 MLAQQRGDAYANADVRVSLEEIACKQGHDDVSKLTPTDIAIESLHKIE 278
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-!- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
-!- SIMILARITY: Belongs to the shikimate kinase family.
                                                                                                                                                         280 AA; 30473 MW; DGED9087D0AA910A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 44, Last annotation update)
Shikimate kinase (EC 2.7.1.71) (SK).
NamesaroK; OrderedLocusNames=s111669;
Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroccoccales; Synechocystis.
                                                                                                                                                                                     21.7%; Score 331.5; DB 2; 36.8%; Pred. No. 2.4e-17; tive 40; Mismatches 89;
         EMBL; BT012132; AAS76227.1; -.
EMBL; BT012407; AAS92323.1; -.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0004765; F:Bhikimate kinase activity; IES
GO; GO:0004652; P:Bhikimate kinase activity; IES
GO; GO:0008652; P:Bhikimate kinase activity; IES.
InterPro; IPR008162; Pyrophosphatase.
InterPro; IPR0080623; Shik kinase.
PRINTS; PR01100; SHIKIMTENASE.
PROSITE; PS00387; PPASE; UNKNOWN_1.
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MEDLINE=97061201; Pubmed=8905231;
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Matches 84; Conservative
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P72796;
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MEDLINE-22825697; PubMed=12917641; DOI=10.1038/nature01943;

MEDLINE-22825697; PubMed=12917641; DOI=10.1038/nature01943;

Palenik B., Brahamsha B., Larimer F.W., Land M.L., Hauser L.,

Chain P., Lamerdin J.E., Regala W., Allen B.E., McCarren J.,

Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.;

The genome of a motile marine Synechococcus.";

Nature 424:1037-1042(203)

EMBL; BX569695; CAE08717.1; -.

HSSP, PALF67; IRAG.
                                                                                                                PRINTS; PRO1100; SHIKIMTKNASE.
PROSITE; PS01128; SHIKIMATE KINASE; 1.
Aromatic amino acid biosynthesis; ATP-binding; Complete proteome;
Kinase; Transferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15;
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                                                                                                                                                                                                                                                                                                                                                                                              54; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO: 00:0015/1, F.T. binding; IEA.
GO: 00:004765; F:shikimate kinase activity; IEA.
GO: GO:0004765; F:shikimate kinase activity; IEA.
GO: GO:000652; F:transferase activity; IEA.
GO: GO:000662; P:amino acid biosynthesis; IEA.
InterPro; IPR000623; Shik kinase.
PROSITE; PS01128; SHIKIMATE KINASE; L.
COMPLEE proteome; Kinase; Transferase.
SEQUENCE 191 AA; 20601 MW; EE012DEBC113EA97 CRC64;
                                                                                                                                                                                                                                                                SEQUENCE 189 AA; 20697 MW; 41727D4EC6E585D9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synechococcus sp. (strain WH8102).
Bacteria; Cyanobacteria; Chroococcales; Synechococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 RPLLQVENLE-----ERLGNLLAQRQPLYAQADLRFPLQ 160
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                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 1.5e-16;
                                                                                                                                                                                                                                          ATP (Potential)
                                                                                                                                                                                                                                                                                                                                                     44.48; Pred. .v.
tive 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191 AA
                                                                                                                                                                                                                                                                                                                                  20.9%; Score 318.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 25, Created)
HSSP; P10880; 1SHK.
HAMAP; MF 00109; -; 1.
InterPro; IPR000623; Shlk_kinase.
Pfam; PF01202; SKI; 1.
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                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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completed: August 25, 2005, 11:12:36
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                                             Q7V904
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07V904
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91 LNGRCIYLVGMMGSGKSTVGKIMSEVLGYSFFDSDKLVEQAVGMPSVAQIFKVHSEAFFR 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=2225144; PubMed=12240834;
Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S., Nakamura A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
"Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
DNA Res. 9-123-130(202).
-! CATALYTIC ACTIVIY: ATP + shikimate = ADP + shikimate 3-phosphate.
-!- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAMAP, MF 00109; -; 1.
InterPro; TPR001623; Shik_kinase.
InterPro; TPR01202; SKI; 1.
PRIM; PR01100; SKI; INTERFORMSE.
PROSITE; PS01128; SHIKIMATE KINASE; 1.
Aromatic amino acid biosynthesis; ATP-binding; Complete proteome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1; Length 183;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 RPLL-DQPSGDPYAMAFSKLSMLAQQRGDAYANAD--VRVSLEE 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synechococcus elongatus (Thermosynechococcus elongatus).
Bacteria; Cyanobacteria; Chrococcales; Synechococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 23 ATP (By similarity).
183 AA; 20778 MW; 98FAEZEE114CCA32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 20.4%; Score 311.5; DB 1; Best Local Similarity 43.3%; Pred. No. 4.9e-16; Matches 71; Conservative 28; Mismatches 52;
                                                                                                                                                                                10-OCT-2003 (Rel. 42, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) 8. Abitimate Kinase (EC 2.7.1.71) (SK).
Name=aroK; OrderedLocusNames=tlr0882;
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                                          255 KQGHDDVSKLTPT 267
                                                                    168 LAVADGILQLLPS 180
                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kinase; Transferase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73 TMESQVLNAIGQRHSLVVATGGGIVSKPENWGVLHQGIVIWLNPGREELLRRL-NADSGN
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                                                                                                                                                                                                                                                                                                            MEDLINE=22835698; PubMed=12917642; DOI=10.1038/nature01947; Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P., Rocap G., Larimer F.W., Lamerdin J.E., Malfatti S., Chain P., Allyren N.A., Arellano A., Coleman M., Hauser L., Hess W.R., Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A., Webb E.A., Zinser E.R., Chisholm S.W.; "Genome divergence in two Prochlorococcus ecotypes reflects oceanic niche differentiation."; Nature 424:1042-1047(2003).
BMBL: BX572095; CAE20388.1; --.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18.5%; Score 283; DB 2; Length 192; 39.0%; Pred. No. 8e-14; cive 27; Mismatches 64; Indels 2
01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Shikimate kinase (BC 2.7.1.71)
Mane=aroK, OrderedLocusNames=PMT0163;
Prochlorococcus marinus (strain MIT 9313).
Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 AA; 20863 MW; B6F16CC52E622F76 CRC64;
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GO; GO:0004765; F:shikimate kinase activity; IEA.
GO; GO:0008652; P:amino acid biosynthesis; IEA.
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PROSITE; PS01128; SHIKIMATE_KINASE; 1.
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SEQUENCE 192 AA;
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                                                                                                                                                                                                                                             NCBI_TaxID=74547;
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LK 175
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GenCore (c) 1993
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sw model OM protein - protein search, using Run on:

August 25, 2005, 10:55:14; Search time 17 Seconds (without alignments) 1726.242 Million cell updates/sec

Title: Perfect score:

US-10-660-226-10 1526 1 MEAGGVGLALQARAAGFGSS......ADSSASDAQAESQIQRIQTL 305 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* •• Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

shikimate kinase (shikimate kinase X	shikimate kinase h	shikimate kinase h	probable shikimate	shikimate kinase (shikimate kinase -	probable arok prot	hypothetical prote	shikimate kinase (shikimate kinase I	shikimate kinase I	shikimate kinase (shikimate kinase C	shikimic acid kina	shikimate kinase I
C98025	D82693	AE1293	AC1665	E86973	A81382	A75478	G70658	D84769	KIECS	F90683	B85534	139782	B72004	E64539	CRESO
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11.5	11.4	11.3	11.3	11.2	11.2	10.6	10.4	6.6	8.6		8.6	9.6	9.3		6.5

ALIGNMENTS

probable shikimate kinase precursor [imported] - Arabidopsis thaliana probable shikimate kinase precursor [imported] - Arabidopsis thaliana (Governose ar cress)

C;Species: Arabidopsis thaliana (Mouse-ear cress)

C;Date: 0.2-feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: A84607

M; Koo, H; Moffat, K.S.; Cronin, L.A.; Shen, M; VanAken, S.E.; Umayam, L.; Tallon, Leuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUD: 20083487; PMID: 10617197

A;Residues: preliminary

A;Molecule type: DNA

A;Residues: 1-292 <STO>

A;Residues: 1-292 <STO>

A;Cross-references: UNIPROT: Q9SJ05; GB: AB002093; NID: 94417286; PIDN: AAD20411.1; GSPDB: G;Cgenetics: Context of the plant Arabidopsis characterics context of the plant Arabidopsis characterics.

A; Gene: At2g21940

A; Map position: 2 C; Superfamily: shikimate kinase; shikimate kinase homology

ä Gaps ä DB 2; Length 292; Indels Query Match 42.6%; Score 649.5; DB 2; Best Local Similarity 62.1%; Pred. No. 9.8e-45; Matches 128; Conservative 36; Mismatches 41;

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139 QIFKVHSEAFFRDNESSVLRDLSSMRRLVVATGGGAVIRPINWRYMKRGLSVWLDVPLDA 198 ઠે

199 LARRIAKVGTASRPLLDQPSGDPYAMAFSKLSMLAQQRGDAYANADVRVSLEEIACKQGH ò

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207

208 LAHRIAAVGIDSRPLLHDESGDAYSVAFKRLSAIWDERGEAYTNANARVSLENIAAKRGY 267 a

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Iriguchi Tabata, S

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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Reference in preliminary
A;Residues: 1-181 «KUR»
A;Residues: 1-181 «KUR»
A;Residues: 1-181 «KUR»
A;Coss-references: UNIPROT:Q8YXG9; GB:BA000019; PIDN:BAB73201.1; PID:g17130591; GSFDB:GCGenetics:
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr1244
C;Superfamily: shikimate kinase; shikimate kinase homology
                         C;Accession: A11961
C;Accession: A11961
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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Best Local Similarity
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CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiSpecies: Arabidopsis thaliana (mouse-ear cress)
CiSpecies: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
CiAccession: T09370
RiBevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X submitted to the Protein Sequence Database, June 1999
A;Reference number: Z16652
A;Accession: T09370
A;Accession: T09370
A;Accession: T09370
A;Accession: Colore I and A;Accession: Colore I and A;Accession: Colorectics: CiCore-references: UNIPROT: COSVA4; EMBL: ALO78620; GSPDB:GN00062; ATSP:F23K16.170
A;Gene: ATSP:F23K16.170
A;Gene: ATSP:F23K16.170
A;Gene: ATSP:F23K16.170
A;Map position:
C;Gene: ATSP: F23K16.170
A;Map position:
C;Superfamily: shikimate kinase; shikimate kinase homology
                                                                                                                                          Cross-references: UNIPROT:000497; EMBL:X63560; NID:919348; PIDN:CAA45121.1; PID:919349; Shikimate kinase, shikimate kinase homology; Schorfanily: shikimate kinase, shikimate kinase homology; Keywords: aromatic amino acid biosynthesis; ATP; chloroplast; magnesium; phosphotransf; 103-216/Domain: shikimate kinase homology SKI.>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PINWRYMKRGLSVWLDVPLDALARRIAKVGTASRPLL-DQPSGDPYAMAFSKLSMLAQQR 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 GGITVAEIFBLRGESPFRDNETEVLHKLSLAHRLVVSTGGGAVVRPINWRHMHKGISVWL 203
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                                                                                                                                                                                                                                                                                                                                                                                             73 SVDEALLLKRKSEEVLFYLNGRCIYLVGMMGSGKSTVGKIMSEVLGYSFFDSDKLVEQAV
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                                                                                                                                                                                                                                                                                    Length 300;
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28.1%; Score 429; DB 2; Length 305;
Best Local Similarity 53.3%; Pred. No. 5.6e-27;
Matches 88; Conservative 28; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GDAYANADVRVSLEEIACKQGHDDVSKLTPTDIAIESLHKIESFV 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GEAYTKASARVSLENITLKLGYRSVSDLTPAEIAIEAFEQVQSYL 293
                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                  Query Match 42.1%; Score 642.5; DB 1; Best Local Similarity 60.3%; Pred. No. 3.7e-44; Matches 126; Conservative 35; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      264 ALKR-EKDVCHITPABITLEVLIQIENFL 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACKQGHDDVSKLTPTDIAIESLHKIESFV 281
        Reference number: S21584
     A, Reference number: S2158
A, Accession: S21584
A, Status: preliminary
A, Molecule type: mRNA
A, Residues: 1-300 < SCH>
A, Cross-references: UNIPR
C, Superfamily: shikimate
C, Keywords: aromatic amin
F;103-216/Domain: shikima
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R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; o, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-189 <KAN>
A;Cross-references: UNIPROT:P72796; EMBL:D90900; GB:AB001339; NID:g1651768; PIDN:BAA1681
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: shikimate kinase; shikimate kinase homology keywords: aromatic amino acid biosynthesis; ATP; magnesium; phosphotransferase;11-123/Domain: shikimate kinase homology <SKI>
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                                                                                                                    150
                                                                                                                                                                                                                                         210
                                                                                                                                                                                                                                                                           64 QIESDVLAQVCSYTKLTVATGGGIVLRRENWSYLHHGLILWLDVPVDILYARLA--ADTT 121
                                                                                                                                                                                                                                                                                                                                                                RPLL--DQPSGDPYAMAFSKLSMLAQQRGDAYANADVRVSLEEIACKQGHDDVSKLTPTD 268
                                                                                                                                                                                                                                                                                                                                                                                                                            -----AEETPEQ 162
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                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S74659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 INGRCIYLVGMMGSGKSTVGKIMSEVLGYSFFDSDKLVBQAVGMPSVAQIFKVHSEAFFR
                                                                                                                    LNGRCIYLVGMMGSGKSTVGKIMSEVLGYSFFDSDKLVEQAVGMPSVAQIFKVHSEAFFR
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 shikimate kinase (EC 2.7.1.71) aroK - Synechocystis sp. (strain PCC 6803)
N;Alternate names: hypothetical protein s111669
                                                           25;
   Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 189;
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                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                            122 RPLLODDDPKG-----KÜRSLLEGRTPLYSQADLRICVN----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: S74322; MUID:97061201; PMID:8905231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 318.5; DB 1;
Pred. No. 2.3e-18;
; Score 338.5; DB 2; Pred. No. 5.3e-20; 33; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 44.4%; Pred. No. 2...
Matches 71; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IAIESLHKIESFVIEHTADS 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              || : : | | :: || :
163 IANKVMQAIPS-VLKQTASN 181
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shikimate kinase [imported] - Nostoc sp. (strain PCC 7120) C,Species: Nostoc sp. PCC 7120 A,Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

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CjAccession: F87621
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Dukkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolor
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Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Reaidues: 1-200 <STO>
A;Cross-references: UNIPROT:Q9A435; GB:AE005673; NID:g13424646; PIDN:AAK24970.1; GSPDB:C
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C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession Ab0019
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B
Geno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
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                                                                                                                                                                                                                       156 VLRDLSSMRRLVVATGGGAVIRPINWRYMKRGLSVWLDVPLDALARRIAKVGTASRPLLD 215
                                                                                                                                                                                                                                                             QPSGDPYAMAFSKLSMLAQQRGDAYANADVRVSLEEIACKQGHDDVSKL----TPTDIAI 271
                                                                                                                                                                                                                                                                                                                                                                                                         EGK------BRIREIWEKKKOFYÅ-----EFRRI------DTSRLNEWETTALVVL 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGERRVIARLLDEPPHVLATGGGAFVNAETRALIN----EKAVSVWLKADVELLARRVSR 143
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                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                shikimate kinase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
                                                                                                                                        91 LNGRCIYLVGMMGSGKSTVGKIMSEVLGYSFFDSDKLVEQAVGMPSVAQIFKVHSEAFFR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15.4%; Score 234.5; DB 2; Length 200; 36.0%; Pred. No. 1.4e-11; rative 31; Mismatches 59; Indels 31
                                      IndelB
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   2.6e-11;
         Pred. No. 2.6e
; Mismatches
         Similarity 34.4%; Pro 66; Conservative 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68; Conservative
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PHMVAVEAI 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESLHKIESFVIE
   Best Local Similarity
Matches 66; Conserv
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Best Local Similarity
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A.Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A.Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A.Reference number: A72200; MUID:99287316; PMID:10360571
A.Acession: B72389
A.Status: preliminary
A.Rolleria: DNA
A.Residues: 1-492 <ARN>
A.Cross-references: UNIPROT:Q9WXI3; GB:AE001715; GB:AE000512; NID:g4980839; PIDN:AAD3543
A.Cross-references: strain MSB8
C.Geneeics:
A.Gene: TM0348
F.116-492/Domain: 3-dehydroquinate synthase homology <DGS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 392, 353-358, 1998

A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A;Reference number: A70300; MUID:98196666; PMID:9537320

A;Reference number: A70487

A;Reference number: A70487

A;Rolecule type: DNA

A;Ross-references: UNIPROT:067925; GB:AE000776; NID:g2984355; PIDN:AAC07875.1; PID:g298

A;Ross-references: Strain VF5

A;Genetics:

A;Genetics:

A;Genetics:

A;Genetics:

A;Genetics:

A;Coperterion:

A;Roperfamily: Shikimate kinase; Shikimate kinase homology
                                                                                                                                                                                                                                                                                                                                             C;Species: Aquifex aeolicus
C;Date: OB-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C;Accession: A70487
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov
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R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
| |: | |:: | |:| || || || || || DESTEVLGHIAAQTRSVIATGGGVVLRRQNWSYLHHGLVIWLDGSLELLLARLQ--GDEA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 IYLVGMMGSGKSTVGKIMSEVLGYSFFDSDKLVEQAVGMPSVAQIFKVHSEAFFRDNESS 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156 VLRDLSSMRRLVVATGGGAVIRPINWRYMK-RGLSVWLDVPLDALARRIAKVGTASRPLL 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 VLKDLSEKENVVISTGGGLGANEBALNFMKSRGTTVFIDIPFEVFLERCK--DSKERPLL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  215 DQPSGDPYAMAFSKLSMLAQQRGDAYANADVRVSLEEIACKQGHDDVSKLTPTDIAIESL 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 IYLIGFMCSGKSTVGSLLSRSLNIPFYDVDEEVQKREGL-SIPQIFEKKGEAYFRKLEFE 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      - Thermotoga maritima (strain MSB8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species: Thermotoga maritima
Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                      ;Species: Aquifex aeolicus
;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15.6%; Score 237.5; DB 2; Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                               RPLLDQPSGDPYAMAFSKLSMLAQQRGDAYANADVRVSLE 250
                                                                                                                                                        127 RPLLOVENLE-----ERLGNLLAOROPLYAOADLRFPLO 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 16.3%; Score 249.5; DB 2; Best Local Similarity 33.7%; Pred. No. 6.9e-13; Matches 62; Conservative 34; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 7
B72389
shikimate kinase/3-dehydroquinate synthase
                                                                                                                                                                                                                                                                                                                   shikimate kinase - Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    275 HKIE 278
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C;Accession: F81038; H81984
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. H;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; if, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Accession: F81038
                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: LNA
A;Molecule type: LNA
A;Molecule type: LNA
A;Experimental source: serogroup B, strain MC58
A;Experimental source: serogroup B, strain MC58
B;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell;
Holrody, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-170 <PAR>
A;Cross-references: GB:AL162753; GB:AL157959; NID:g7379120; PIDN:CABB3937.1; PID:g737937
A;Experimental source: serogroup A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gibberies: Salmonella enterica subsp. enterica subsp. enterica serovar Typhi (stra Gibberies: Salmonella enterica subsp. enterica serovar Typhi his species: Salmonella enterica subsp. enterica serovar Typhi his objecties has also been called Salmonella typhi ciparte: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 Cipacession: AC1000 R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001 P.
Nature 413, 848-852, 2001 P.
Nature 413, Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K., A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov A;Reference number: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: A81775; MUID:2022556; PMID:10761919
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A;Molecule type: DNA
A;Residues: 1-173 < PAR>
A;Cross-references: GB:AL513382; PIDN:CAD08127.1; PID:g16505106; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 NGRCIYLVGMMGSGKSTVGKIMSEVLGYSFFDSDKLVEQAVGMPSVAQIFKVHSEAFPRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 NESSVIRDLSSMRRLVVATGGGAVIRPINWRYM-KRGLSVWLDVPLDALARRIAKVGTAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 RPLLQ--VADPLA----KIRELYAARDPVYRQTADFTV--ESANCRE 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 14.2%; Score 217; DB 2; Length 170; Best Local Similarity 37.1%; Pred. No. 2.9e-10; Matches 62; Conservative 30; Mismatches 61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 173;
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A;Gene anok
C;Superfamily: shikimate kinase; shikimate kinase homology
C;Keywords: phosphotransferses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: shikimate kinase; shikimate kinase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 217; DB 2;
Pred. No. 3e-10;
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32.4%;
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Best Local Similarity
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Accession: 02.5.7 (Control of the Control of the Co
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C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       shikimate kinase VC2629 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 RCIYLVGMMGSGKSTVGKIMSEVLGYSFFDSDKLVEQAVGMPSVAQIPKVHSEAFFRDNE 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94 RCIYLVGMMGSGKSTVGKIMSEVLGYSFFDSDKLVEQAVGMPSVAQIFKVHSEAFFRDNE 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 SSVLRDLSSMRRLVVATGGGAV-IRPINWRYMKRGLSVWLDVPLDALARRIAKVGTASRP 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Vibrio cholerae
Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
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Matches 60; Conserv
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R; Heidelberg, J.F.;
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C; Species: Escherichia coli
C; Species: Becherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 24-Aug-2001
C;Accession: H91157
R;Hayashi, T:; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishli, K.; Yokoyama, K.; Han, C.G
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gen.
A;Reference number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               shikimate kinase I [imported] - Escherichia coli (strain O157:H7, substrain RIMD 050995.
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C;Species: Escherichia coli
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                                                                                                                                                                                                                                                                                                                                            72 RNIFLVGPMGAGKSTIGRQLAMEFYDSDQEIEKRTG-ADVGWVFDLEGEEGFRDRE 130
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189 LLHVETPPRE-----VLEALANERNPLYEEIADVTIRTDDQSAKV-----V 229
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A;Residues: 1-240 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB37655.1; PID:g13363706; GSPDB:GN00154
A;Experimental source: strain 0157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LL--DQPSGDPYAMAFSKLSMLAQQRGDAYAN-ADVRVSLEEIACKQGHDDVSKLTPTDI 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 EKVINELTEKQGIVLATGGGSVKSRETRNRLSARGVVVYLETTIEKQLARTQR--DKKRP
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                                                                                                                                                                                       Length 240;
                                                                                                                                                                                                                                                67; Indels
                               A;Map position: 27 min
C.Superfamily: shikimate kinase; shikimate kinase homology
C;Keywords: phosphotransferase
F;70-183/Domain: shikimate kinase homology <SKI>
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Best Local Similarity 31.6%; Pred. No. 5.5e-10;
Matches 60; Conservative 37; Mismatches 67
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A;Gene: EC84232
C;Superfami
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A.Accession: A65144
A.Accession: A65144
A.Accession: A65144
A.Accession: A10 cellary: nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Greadidues: 1-240 cellary:
A.Greadidues: 1-240 cellary:
A.Accession: A10 cellary:
A.Accession: A10 cellary:
A.Accession: A1143
A.Acce
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C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Date: 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A65134; I41143; 549529; A41967; S25243; S31741
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
A,; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;File: The complete genome sequence of Escherichia coli K-12.
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A;Rebidues: 'MRPOPMSCRA',50-164,'ALSFILKRPSKSNLHARSG' <LOB2>
A;Cross-references: EMBL:M76389; NID:g145379; PIDN:AAC36834.1; PID:g145380; EMBL:Z19601;
C;Genetics:
      7;
                                                            94 RCIYLVGMMGSGKSTVGKIMSEVLGYSFFDSDKLVEQAVGMPSVAQIFKVHSEAFFRDNE 153
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                                                                                           154 SSVLRDLSSMRRLVVATGGGAV-IRPINWRYMKRGLSVWLDVPLDALARRIAKVGTASRP
      Gaps
      22;
      Indels
      69;
   Mismatches
   36;
   Conservative
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QIIHMLES 172
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C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C;Accession: F86003
F;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: F86003
A;Status: preliminary
A;Accession: F86003
A;Actus: DNA
A;Residues: 1-240 <5TO>
A;Coss-references: GB:AE005174; NID:g12518013; PIDN:AAG58490.1; GSPDB:GN00145; UWGP:247
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Genetics:
A;Genetics: Accession axok
C;Superfamily: shikimate kinase; shikimate kinase homology
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14.2%; Score 216; DB 2; Length 240;
Best Local Similarity 31.6%; Pred. No. 5.5e-10;
Matches 60; Conservative 37; Mismatches 67; Indels
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230 ANQIIHMLES 239
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